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SEARCH REQUEST FORM

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Scientific and Technical Inf rmation Center

	75201			
Requester's Full Name: M.A.W Art Unit: 1652 Phone N Mail Box and Bldg/Room Location 10 D0 I f more than one search is subm	ALICKA Tumber 30 5 - 727 10 D 0 6 Resu itted, please prioritiz	its Format Preferred (cir e searches in order of	f need.	<u>1002</u> 3 K E-MAIL
Please provide a detailed statement of the nclude the elected species or structures, k atility of the invention. Define any terms known. Please attach a copy of the cover s	search topic, and describe a eywords, synonyms, acron that may have a special me theet, pertinent claims, and	s specifically as possible the yms, and registry numbers, a aning. Give examples or rel abstract.	e subject matter to be s and combine with the c levant citations, author	concept or
Title of Invention:	Propriori la.	eterum Vec	for	
inventors (please provide full names):	Pieter	Pouwels	et al	
Earliest Priority Filing Date: *For Sequence Searches Only* Please includes ppropriate serial number.	6 25 99 de all pertinent information ()	parent, child, divisional, or issu	ued patent numbers) alo	ng with the
Please search Thank you so	much in	_	(7 - 1-100 - 100 -
	VW W		Point of Contact: Toby Port Inical Info. Specialist CM1 6A04 703-308-3534	
STAFF USE ONLY Searcher: Searcher Phone #: Searcher Location: Date Searcher Picked Up:	Type of Search NA Sequence (#) AA Sequence (#) Structure (#) Bibliographic	Vendors and co		
Date Completed:	Litigation	Lexis/NexisSequence Systems		-
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Other (specify)_

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ALIGNMENTS

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DEFINITION
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AUTHORS
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Sequence 1 from Patent BP09728357
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Propionibacterium freudenreichii
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Propionibacterineae;
Propionibacterium.
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Pouwels, P.H., Jore, J.P.,
Propionibacterium vector
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Result No.

Score

Query Match Length DB

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Description

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SUMMARIES

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Jore, J. P., Luiten, R.G., Pouwels, P.H. and Van Luijk, N. Propionibacterium vector
Patent: WO 9967356-A 1 29-DEC-1999;
GIST BROCADES BV (NL); JORE JOHANNES PETRUS MARIA (NL);
NICOLE VAN (NL); LUITEN RUDOLF GIJSBERTUS MARIE (NL);
PIETER HENDRIK (NL)
                                                                                                                       Propionibacterium freudenreichii.
Propionibacterium freudenreichii
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TVSDFWPPDSWQRTKRKNPVGLGRNCTLFETTVEWDVYEVCVESGSATWTPRPEDRHDL
KQRSSICARRVTEFSALPASILRATIRSFYKWITTRYTGWLDSRTTSEEKSAAYHRN
TGRQGGLKGGLASAKLAARPPASALWRQSAMATRERIFVMG"
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/VQAVSRSASTYSTSAVSPSTSTRSASTSERNWSRSGVTAARAAR"
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DKLNERITTLLE"
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Query Match Best Local S Matches 552

al Similarity 552; Conserv

3.4%; ilarity 48.2%; Conservative

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Propionibacterium acidi-propionici
Propionibacterium acidipropionici
Bacteria; Firmicutes; Actinobacteria; Actinobacteria; Actinomycetales; Propionibacterineae; Propionibacterineae;
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Propionibacterium acidi-propionici
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Yamadaoka, Suita, Osaka 562, Japan
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Submitted (13-OCT-1997) Yoshikatsu Murooka, G
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tctggggccccgcagacgc---
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LHAVIASTVEALNAGYSEPLPAREAAGIAASIHRWITHRFYGWIDSHTVNEATFSTIQ
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Pred. No. 8.1e-11;
0; Mismatches 273;
-gctctacgagctgcgcgccctcgcacacaccctcg
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Propionibacterium jensenii plasmid
ORF6 and ORF7, ORF8, ORF9 and PpnA.
AJ250233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium jensenii
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Propionibacterineae;
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-OCT-1999) Stierli M.P., Microbiology, LFO G16, ETH Zuerich, Ir Schmelzbergstrasse 9, CH-8092 Zuerich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stierli, M.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stierli, M.P., Meile, L. and Teuber, M. Molecular analysis of plasmid pLME106, Propionibacterium jensenii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        syst. Appl. Microbiol.
20383893
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PpnA gene; theta replicase
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155. .388
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                                                                                                /note="ORF10"
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                                                     tcggccgcaacgtcaccctgttcgacaccacccgcatgtgggcataccgggccgtccggc
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Pred. No. 8.1e-11;
0; Mismatches 273;
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AY004211
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Moore, M.W., Bowling, D. and Glenn, D.
Nucleotide sequence of a plasmid from Brevibacterium linens:
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Moore, M.W., Glenn, D. and Bowling, D.
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a 2349 c 2133 g 1555 t 2 others
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	ccgaaac	1035	γ
		4751	밁
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	GTGGGACTCGGCCGTAACTGCACCCTCTTCGAGACCGTCCGGGTGGGACGTGTACCGGGTC 4630	4571	Db
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	GANAACCCTGCCAACGCCAACGCCCACGCCGTGTGGGCACTCGCGGAGCCTGTCACCCGC 4330	4271	ДЪ
	aaccytytcacyaccaccygacacatcytctatyccttyaayaaccctytytytcty 563	507	QΨ
	CGACGCGCTCATGCGCGCATGTGGAACCGGAAAGCCTGGCAACCCAATGCCATCG	4211	뫄
	tcggatgctgactgggccgcagacctcgctgggctgccttcaccgtcctacgtgtccatg 506	447	δō
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	cgtcagccgagaagtctggggcgtaccggcacgtgactcggcagaggggcgctggagctg 386	327	δõ
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	tggctgccacgcaagcc	270	QΥ
	CCAAGTTTGAACACCCGCGTGAAGTCCAACGCTGAACGGCACTCATGTGTGAGTGTGGG 4030	3971	В
	atygaccacyctyaacytyactcycatycttcact	210	Qγ
6;	y Match 3.2%; Score 112.6; DB 1; Length 7610; Local Similarity 46.9%; Pred. No. 7.3e-10; hes 595; Conservative 0; Mismatches 629; Indels 45; Gaps	Query Match Best Local Matches 59	

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Ryabchenko, L.E., Nov
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Rhodococcus erythropolis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                          /translation="MKSATGGVLSDRQWADAVLLPHRPFATNNLQRGQYRMSRDDALA
MRYVEHSPHALLGSIVIDCDHVDAAMRAFEQPSDHPAPNWVAQSPSGRAHIGWWLGPN
HVCRTDSARLTPLRYAHRIETGLKISVGGDFAYGGQLTKNPIHPDWETIYGPATPYTL
RQLATIHTPRQMPRRPDRAVGLGRNVTMFDATRRWAYPQWWQHRNGTGRDWDHLVLQH
                                                                                                                                                              rhodochrous pRC4 putative replication protein (repA), Rhodococcus rhodochrous pKA22 putative theta replicase (ORF2), Rhodococcus erythropolis pFAJ600 putative replication protein (repA), Mycobacterium fortuitum pAJ600 putative replication protein (37K)"
   CHAVNTEFTTPLPFTEVRATAQSISKWIWRNFTEEQYRARQAHLGQKGGKATTLAKQE
AVRNNARKYDEHTMREAII"
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/db_xref="GI:11095365"
                                                                                                                                                                                                                                                                         /plasmid="pN30"
/db_xref="taxon
                                                                                                                                     /transl_table=11
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                                                                                                                                                                                                                                       /note="ORF1; putative; similar to putative Rhodococcus
                                                                                                                                                                                                                                                                                                     organism="Rhodococcus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-MAR-2000) Kenji Maruhashi, Petroleum Energy Center, Bio-Refining Process Laboratory; Sodeshi-cho 1900, Shimizu, Shizuoka 424-0037, Japan (E-mail: M. maruebrpl. pecj.or.jp, Tel:+81-543-67-9550, Fax:+81-543-67-9552)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hirasawa,K., Ishli,Y., Kobayashi,M., Kolzumi,K. and Maruhashi,K. Improvement of desulfurization activity in Rhodococcus erythropolis KA2-5-1 by genetic engineering Biosci. Biotechnol. Biochem. 65 (2), 239-246 (2001)
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Ishii,Y., Hirasawa,K. and Maruhashi,K.
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/gene="repA"
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2052. .:
   /translation="MGAETPARRTRTAREVAERIGASPRTVRRIIAEPRASYEARAAE
RRKQVLELRASGMKLREIAAEVGMSVGGVGTILHHARKTEQSKAEGAMA"
a 828 c 755 g 475 t
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/db_xref="GI:7262573"
                                                        /product="DNA-binding replication
/protein_id="BAA92819.1"
/db_xref="GI:7262574"
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/transl_table=11
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                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteria Actinomycetales; Micrococcineae; Brevibacteriaceae; 1 (bases 1 to 1746)
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Brevibacterium linens
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 Ankri,S.,
                                                                       Corynebacterium glutamicum Plasmid 36 (1), 36-41 (1996)
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tcacgaccaccggacacatcgtctatgccttgaagaaccctgtgtgtcttgaccgatgccg
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                                                                                                              AGGCCAACCCACAATCCTTGTCGAATCTCCTCGTCGTCGACATCGACCACCCCGACGCGC
                                                                                                                                          aagcgaacccgttggtcatgcagtccttggtcatcaccgatcgagatgcttcggatgctg
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Submitted (02-NOV-1995) Serge Ankri, Centre National de la
Recherche Scientifique, Institut de Genetique Moleculaire (URA
1354) Universite Paris-Sud Batiment 409, Piece 206, Orsay, 91405,
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693. .7
725. .7
797. .8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-*orf310; putative theta replicase; indispensable for pRBLI plasmid replication in C.glutamicum; similar to proteins of C.glutamicum pXZ10142 plasmid, PIR Accession Number S3Z701 and Mycobacterium fortuirum pAL5000 plasmid, PIR Accession Number JQ1440; shares some common motifs with replicases from the Shigella sonnel CoLE5-099, encoded by GenBank Accession Number D30060 and from Streptococcus pyogenes pSM19035, encoded by GenBank Accession Number X61167; Method: conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="aab03568.1"
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/plasmid="autonomous circular plasmid
/strain="RBL"
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Submitted (04-AUG-1995) Jose A. Ainsa, Dep
Biologia Molecular, Facultad de Medicina,
y Cantabria, Zaragoza/Santander, Spain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ainsa,J.A., Martin,C., Cabeza,M., De la Cruz,F. and Mendiola,M.V. Construction of a family of Mycobacterium/Escharichia coll shutil vectors derived from pAL5000 and pACYC184: their use for cloning antibiotic-resistance gene from Mycobacterium fortuitum Gene 176 (1-2), 23-26 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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QDIALATRDJAEELGGEWADRFLVLYGIAAPDSQRIAFYRLDEFF"
2665. 5252
/organism="Plasmid pal5000"
/note="Ecorv/Hpal from pal5000; minimal mycobacterial
replicon from pal5000, GenBank Accession Number M23557"
/db_xref="taxon:2522"
/db_xref="taxon:2522"
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I31848
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1 (bases 1 to 6407)
Stover, C.K.
Bacterial expression vectors
signals of lipoproteins
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Stover, C.K.
Bacterial expression vectors containing
signals of lipoproteins
Patent: US 5583038-A 1 10-DEC-1996;
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I31863
                                                         Bacterial expression vectors containing signals of lipoproteins Patent: US 5583038-A 20 10-DEC-1996;
                                                                                                Unclassified.
1 (bases 1 to 4120)
Stover, C.K.
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Stover,C.K.
Bacterial expression vectors containing signals of lipoproteins
Patent: US 5583038-A 21 10-DEC-1996;
Location/Qualifiers
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Query Match
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Mismatches

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                                                       GTCAGCAGACCACGTACAAAGCGGCTCCGACGCCGCTAGGGCGGAATTGCGCACTGTTCG 1200
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Search completed: October 6, 2002, 15:18:28 Job time: 14006 sec

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Minimum DB
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Copyright (c) 1993 - 2000
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4505	4352	4296	4120	4120	6407	1463	1382	3555	Query Match Length DB
17	17	17	18	13	18	19	19	21	BE
AAT28276	AAT28273	AAT28272	AAT64421	AAQ21502	AAT64413	AAV69312	AAV69313	AAZ49691	ij,
Plasmid pMV261 seq	Plasmid pMH29 sequ	Plasmid pMH28 sequ	Plasmid pMV206. S	Vector pMV206 for	plasmid pMV101. s	M. fortuitum plasm	M. fortuitum plasm	Propionibacterium	Description

25-JUN-1999; 29-DEC-1999. WO9967356-A2

99WO-EP04416

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
46.6	46.6	46.6	47	47	47	47	47.4	47.4	48.2	48.2	48.2	49.4	49.4	49.8	50.2	50.2	50.2	50.2	50.2	50.2	50.2	52.4	52.4	56.2	56.2	56.2	56.2	56.2	58.6	58.6	68.6	68.6	77.4	80.6	80.6
1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	4	4	4	5	G	σ	σ	1.6	1.6	1.6	1.6	1.6	1.9	1.9	2.2	2.3	2.3
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AAZ87285	AAZ87318	AAZ87298	AAA14651	AAI58196	AAK51846	AAS44991	AAA58471	AAD17185	AAQ64201	AAZ48297	AAQ64203	AAC55841	AAC55844	AAS18436 ·	AAA14651	AAA14662	AAA14664	AAA14661	AAA14663	AAF74817	AAZ09259	AAD17186	AAD17184	AAA14669	AAA14667 .	AAA14668	AAA14665	AAA14666	AAQ31727	AAQ31743	AAQ41316	AAQ41331	AAT28281	AAT28279	AAT28278
		S. venezuelae macr			Human polynucleoti	cDNA encoding nove	Nucleotide sequenc	Streptomyces nours	Sequence comprisin	S. coelicolor Yesw	snaß gene encoding	Complete Mitomycin	Mitomycin gene clu					Nucleotide sequenc	Nucleotide sequenc	Rice cDNA sequence	Rice RPC213 cDNA.							tide	٠ ص	ı و	ı	- casse			Plasmid pMH30-lux

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium plasmid LMG 16545 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Propionibacterium LMG 16545 protein-1"
/note= "Encoded by ORF-1"
1181...1438
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/note= "Encoded by ORF-2"
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Query Match
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ccttgaagaaccctgtgtctgaccgatgccgcgcggcgacggcctatcaacctgctcg
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DB; AAY44636, AAY44637.
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                                                     acatggcggcgtgcgaaggccttcggcgcgccgtcgacggcgaccgcagttactcag
                                                                              tgctcgccgcgtcgagcagggcctatgcgacgttctcggcggcgatgcatcctacgggc
                                                                                                                                                     tctatgccttgaagaaccctgtgtgtctgaccgatgccgcgcgggcgacggcctatcaacc
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Pred. No. 3.9e-10;
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                                                                                                                                                                                                                                                          This genomic DNA sequence contains is the Mycobacterium fortiutum plasmid pAL 5000 origin of replication, ori. This sequence is used in a method which results in the formation of Mycobacterium recombinant
                                                                                                                                                                                                                                                                                                                                                               Recombinant non-pathogenic Mycobacterium as vaccines providing long term cellular immunity - useful against intracellular pathogens, cancer and autoimmune disease, and are retained in host macrophages
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Best Local Similarity 47.8%; Matches 274; Conservative

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                                                                     /note= "Supports 5258..6073
                                                                                                                                                                                                                                    complement (1598..2542)
/*tag= a
                                                                                                                                                                 /note= "Supports autonomous
complement (1954..3060)
  /mod_base= kan
/note= "Kanamy
                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                      Location/Qualifiers
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  "Kanamycin
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Matches 274
                                                                                                                                                                                                                                                                   This sequence represents the plasmid pMV101. This plasmid was used in the construction of a series of vectors used to produce the recombinant Mycobacteria of the invention. The recombinant mycobacteria of the invention are transformed with DNA encoding a polypeptide which comprises a lipoprotein secretion signal sequence and an antigen (Ag) heterologous to the mycobacteria. The lipoprotein secretion signal causes the Ag to be produced as a lipoprotein. The mycobacteria may be used in the form of a live bacterial vaccines against Lyme disease, where the bacterial express a surface protein of Borrelia burgdorferi, the causative agent of Lyme disease.
                                                                                                                                         2852
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacteria expressing secretion signal of lipoprotein and heterologous antigen, esp. outer surface protein A or B of Borrelia burgdorferi - are used in the form of a live bacterial vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-042315/04.
P-PSDB; AAW14834-36.
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21-OCT-1991;
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Local Similarity 47.8%;
nes 274; Conservative
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             tgccttcaccgtcctacgtgtccatg-----aaccgtgtcacgaccaccggacacatcg
                                                                                       AGCTCTGGCTGCCGTACTGGCCGCTGGCAAGCGACCATCTGCTCGAGGGGATCTACCGCC
                                           ACCTGCTGGTCGTGGACGTAGACCATCCAGACGCAGCGCTCCGAGCGCTCAGCGCCCCGGG
                                                           ccttggtcatcaccgatcgagatgcttcggatgctgactgggccgcagacctcgctgggc
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/note= "Fragment c
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; Pred. No. 6.3e:
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site-specific integration;
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/note- "kanamycin ı
1220..2011
                           91WO-US04833
                                                                                                                                                                                                                                                                                                              /note- "M.rep cassette" 3925..4016
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2012..2025
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/product= KanR
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                                                                                                                                                                                                                                                           'function= Multiple_cloning_site
                                                                                                                                                                                                                                                                                                                                                                                                                     'note- "MluI-NotI linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21..936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cassettes of all the components necessary for plasmid replication in E.coli and mycobacteria (E.rep and M.rep, respectively) and for selection of transformants (KanR) were constructed using the PCR technique. A multiple cloning site was synthesised. The cassettes were constructed to allow directional cloning and assembly into a plasmid where all transcription is unidirectional. Plasmid pMY206 was derived from plasmid pMV204 which was made up of all the cassettes. It was modified by the insertion of an Mull-NotI linker between the M.rep and E.rep cassettes to facilitate removal of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA site-specific integration into Mycobacteria - useful as adjuvant in vaccines and as therapeutic agent for malaria, influenza, herpes and human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jacobs WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUL-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 2.3%;
Local Similarity 47.6%;
nes 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ep in further constructions. 
 {\tt AAQ21568-Q21573} for the PCR primers used in the construction individual cassettes.
acaccaccgcatgtgggcataccgggccgtcc
                                 gtcagcagaccacgtacaaagcggctccgacgccgctagggcggaattgcgcactgttcg
                                                                                                                                                                                                accggatcacaaagaacccgctcagcaccgcccatgcgaccctctggggccccgcagacg
                                                                                                                                                                                                                                                                      tyctcycccycytcyaycayyycctatycyacyttctcygcygcyatycatcctacygyc
                                                                                                                                                                                                                                                                                                                                          tctatgccttgaagaaccctgtgtgtctgaccgatgccgcgcggcggcgacggcctatcaacc
                                                                                                                                                                                                                                                                                                                                                                                          tgccttcaccgtcctacgtgtccatg-----aaccgtgtcacgaccacacggacacactcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acctgctggtcgtggacgtagaccatccagacgcagcgctccgagcgctcagcgcccggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccttggtcatcaccgatcgagatgcttcggatgctgactgggccgcagacctcgctgggc 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgactcggcagagggcgctggcstgccttacatcgaagcgaacccgttggtcatgcagt 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agctctggctgccgtactggccgctggcaagcgatctgctcgaggggatctaccgcc
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                                                       cagggaacccgcgtcgcaacgtcaccgtatccg
                                                                                                                                                                           gcctcatgaccaaaaaccccggccacatcgcctgggaaacggaatggctccactcagatc
                                                                                                                                                                                                                                                                                                                    tgtgggcactcaacgcccctgttccacgcaccgaatacgcgcggcgtaagccgctcgcat 2681
                                                                                                     tctacacactcagccacatcgaggccgagctcggcgcgaacatgccaccgccgcgctggc
                                                                                                                                        cgctctacgagctgcgcgccctcgcacacccctcgacgagatccacgcactgccggagg
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UNIV OF PITTSBURGH.
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pred. No. 1.3e-09;
0; Mismatches 294;
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 867
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RESULT
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                                                                                       This sequence represents the plasmid pMV206. This plasmid was used in the construction of a series of vectors used to produce the recombinant Mycobacteria of the invention are transformed with DNA encoding a polypeptide which comprises a lipoprotein secretion signal a polypeptide which comprises a lipoprotein secretion signal
                                                                                                                                                                                                  Mycobacteria expressing secretion signal of lipoprotein and heterologous antigen, esp. outer surface protein A or B of Borr burgdorferi - are used in the form of a live bacterial vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                              sequence and an antigen (Ag) heterologous to the mycobacteria. The lipoprotein secretion signal causes the Ag to be produced as a lipoprotein. The mycobacteria may be used in the form of a live bacterial vaccines against Lyme disease, where the bacteria express a surface protein of Borrelia burgdorferi, the causative agent of
                                                                                                                                                                  Example 1;
                                                                                                                                                                                         against Lyme disease
                                                                                                                                                                                                                                                    WPI; 1997-042315/04.
                                                                                                                                                                                                                                                                             Stover CK;
                                                                                                                                                                                                                                                                                                                         17-NOV-1992;
21-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
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                                                                                                                                                                                                                                                                                                  (MEDI-) MEDIMMUNE
                                                                                                                                                                                                                                                                                                                                                             21-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                     10-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pMV101; Mycobacteria; antigen; bacterial vaccine; Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pMV206.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                Fig 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                         92US-0977630
91US-0780261
                                                                                                                                                                                                                                                                                                                                                            9108-0780261
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "M.rep
3925..4120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "E.rep cassette"
2012..3920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1..1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacteria; lipoprotein secretion signal al vaccine; Lyme disease; Borrelia burgdor; primer; amplify; PCR; polymerase chain rea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "kan gene"
1220..2011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/note= "NheI/SpeI kan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ′*tag=
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                                                                                                                                                                122pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 "Synthetic multiple cloning site"
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chain reacti
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                                                                                                                                                                                                                Borrelia
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Sequence

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1166 G;

907 T; 0 other;

03-OCT-1994;

94US-0316950

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AAT28272
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AC AAT2
AC 19-A
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Best Local Similarity
Matches 273; Conserv
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                                                                                                                                                              reporter gene; luminescence; BCG; Mycobacterium bovis Mycobacterium tuberculosis; Mycobacterium avium; Mycobacterium intracellulare; Mycobacterium kansasii; Mycobacterium scrofulaceum; Mycobacterium leprae; tub
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                                       02-OCT-1995;
                                                                                                                       Synthetic.
                                                                                                                                                                                                                                              Plasmid pMH28 sequence
                                                                                                                                                                                                                                                                         19-AUG-1996
                                                                                                                                                                                                                                                                                                     AAT28272;
                                                                                                                                                                                                                                                                                                                               AAT28272
                                                                 11-APR-1996
                                                                                            WO9610645-A1
                                                                                                                                                                                                                 Plasmid pMH28; vector; firefly; luciferase; DNA cassette;
                                                                                                                                                                                                                                                                                                                                                                                                                             835
                                                                                                                                                .eprosy; antibiotic; tuberculostatic; vaccine; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       715
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                                                                                                                                                                                                                                                                                                                                                                                                 attccgtcaggttgtgggcctatcgtcccgccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                      luminescence; BCG; Mycobacterium bovis; tuberculosis; Mycobacterium avium;
                                       95WO-US12642
                                                                                                                                                                                                                                                                                                                               DNA;
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Pred.
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No. 1
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L.3e-09;
hes 294;
                                                                                                                                                               tuberculosis;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quantification of mycobacteria by luminescence - using reporter strains contg. a lux gene, permits the determn. efficacy of anti-mycobacterial and prophylactic compsns.
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                      acaccacccgcatgtgggcataccgggccgtcc
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                                                                                                                                                                                                                                                                                     acatggcggcgtgcgcaaggccttcggcgcgcgtcgatggcgaccgcagttactcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tuberculostatic and vaccine compositions.
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Pred. No. 1.4e-09;
0; Mismatches 294;
 2977
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    using bacterial
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RESULT
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                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 273; Conserv
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                                                                                  tgactcggcagagggcgctggagctgccttacatcgaagcgaacccgttggtcatgcagt 420
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Pred. No. 1.4e-09;
0; Mismatches 294;
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This is the complete sequence of plasmid pMV261. This plasmid an extrachromosomal Mycobacterium-Escherichia coli shuttle expression vector. A mutant FFlux firefly luciferase (EC-1.13. reporter gene DNA cassette may be inserted downstream from a
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Plasmid pMH30-lux; vector; firefly; luciferase; DNA cassette; reporter gene; luminescence; BCG; hsp70-tac promoter; Mycobacterium bovis; Mycobacterium tuberculosis; Mycobacterium avium; Mycobacterium intracellulare; Mycobacterium kansasii;

Plasmid 19-AUG-1996

рмн30-lu**x**

sequence

(first

entry)

Mycobacterium intracellulare; mycobacterium leprae; tu Mycobacterium scrofulaceum; Mycobacterium leprae; tu cobacterium leprae; drug

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                                                           tgtgggcactcaacgcccctgttccacgcaccgaatacgcgcggcgtaagccgctcgcat
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                                                                                                                                                       mycobacteria) changed to ATC to enhance expression, into the extrachromosomal Mycobacterium-Escherichia coli shuttle expression vector plasmid pMV261 (AATC8276), downstream from the BCG heat show protein hap60 promoter. Although levels of transformants are low, expression levels are high from the hsp60 promoter. This type of
                                                                                                                                                                                                                                                                                                                                                    Quantification of mycobacteria by luminescence - using k reporter strains contg. a lux gene, permits the determn. efficacy of anti-mycobacterial and prophylactic compsns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pMV261-lux; vector; firefly; luciferase; DNA cassette; reporter gene; luminescence; BCG; hsp60 promoter; Mycobacterium bovis; Mycobacterium tuberculosis; Mycobacterium avium; Mycobacterium intracellulare; Mycobacterium kansasii; Mycobacterium scrofulaceum; Mycobacterium leprae; tuberculosis;
                                            reporter gene expression is detected by luminescence without lysis or cell concentration. The method may determine the efficacy of antibiotic, tuberculostatic
                                                                                                   expression levels are high from the hsp60 promoter. This type of vector may be used in a new method for quantifying Mycobacterium infection in vivo. An animal is injected with e.g. Mycobacterium bovis BCG, etc., transfected with one of these vectors, and
                                                                                                                                                                                                                                             This is the complete sequence of plasmid pMV261-lux. This plasm has been constructed by insertion of a mutant firefly luciferase (EC-1.13.12.7) reporter gene, with an Ile ATA codon (rare in
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                                                The method may be used tuberculostatic and vac
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03-OCT-1994;
                                                                                                  Synthetic
                                                                                                                          Mycobacterium intracellulare; Mycobacterium kansasii; Mycobacterium scrofulaceum; Mycobacterium leprae; tuberculosis; leprosy; antibiotic; tuberculostatic; vaccine; drug screening;
                                                                                                                                                             Plasmid pMV206; vector; firefly; luciferase; DNA reporter gene; luminescence; BCG; Mycobacterium Mycobacterium tuberculosis; Mycobacterium avium;
                                                                                                                                                                                                                                                                                               AAT28281 standard;
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94US-0316950
                        95WO-US12642
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Pred. No. 1.5e-09;
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Length

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This is the complete sequence of plasmid pMV206. This plasmid may the has been used in construction of vectors for use in Mycobacterium to spp. The plasmid may be modified to construct plasmid pPA207SC, to followed by insertion of a multiple cloning site and an Escherichia coli TIT2 terminator sequence, to give plasmid pMH28 (AAT28272) and its derivative plasmid pMH29 (AAT28273). A mutant firefly luciferase (EC-1.13.12.7) reporter gene is inserted to give plasmid pMV30-lux (AAT28278). This type of vector may be used in a new method for quantifying Mycobacterium infection in vivo. An animal is injected with e.g. Mycobacterium bovis BCG, etc., animal is injected with one of these vectors, and reporter gene expression is detected by luminescence in tissues without lysis or cell concentration. The method may be used to determine the efficacy of
                                                                                                                                                                                                                                                                                                                                                                                                             reporter strains contg. a lux gene, permits the efficacy of anti-mycobacterial and prophylactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quantification of mycobacteria by luminescence
Sequence 4120
                                          antibiotic, tuberculostatic and vaccine compositions.
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BP; 921 A; 1126 C; 1166 G; 907 T; 0
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gtcagcagaccacgtacaaagcggctccgacgccgctagggcggaattgcgcactgttgg
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                                                               tctacacactcagccacatcgaggccgagctcggcgaacatgccaccgccgcgctggc
                                                                                   cyctctacgayctycycycctcycacacacaccctcyacyayatccacycactyccyyayy
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8.1e-09;
hes 296;
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Best Local S
Matches 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents that of plasmid pWV206. This is a plasmid containing sequences necessary for replication in mycobacteria. It contains a synthetic multiple cloning site to facilitate versatile molecular cloning and manipulations for foreign gene expressions in mycobacteria and for integration into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expression vector for expressing protein or polypeptide in mycobacterium - contg DNA sequences encoding lipoprotein secretion signal and peptide heterologous to bacteria expression protein of lipoprotein heterologous to bacteria
          2501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mycobacterial
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pertussis; malaria; influenza virus; CTL; herpes virus.
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                                                                                                                                                                                                                                                                                                                     Local Similarity
mes 272; Conserv
                                                                                                                                  tgactcggcagagggcgctggagctgccttacatcgaagcgaacccgttggtcatgcagt
  acctgctggtcgtggacgtagaccatccagacgcagcgctccgagcgctcagcgcccggg
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Pred. No. 1.1e-06;
0; Mismatches 294
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5257..6076
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cytotoxic T-lymphocyte response; transformed Mycobacteria; Mycobacterium smegmatis; vaccine; cell mediated immunity; pertussis; malaria; influenza virus; CTL; herpes virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents that of plasmid pMV101. This is a modified version of plasmid pVUB125, which had 792 bases of the tet gene (inactivated by prior manipulations) deleto. The plasmid represents an expression vector. The HSP61 coding sequence was inserted between the NheI and BamHI sites to form pMV65A. NOTE: When the proteins encoded by this sequence were decoded, the published sequence was found to contain approx. 65 codons which did not code for the amino acids dictated by the universal genetic code. The sequence also contained many insertions and deletions which upset the open reading frame that was displayed as the contain proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expression vector for expressing protein or polypeptide in mycobacterium - conty DNA sequences encoding lipoprotein secretion signal and peptide heterologous to bacteria expressing
                                                                   2434
                                                                                                                                                                                                      2554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoded proteins. The complementary strand was also found to contain many insertions and deletions that did not have corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 5; 86pp; English.
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DB; AAR34542; AAR34543; AAR34544.
GTGAGCAGACCAAGTACAAAGCGGCTCCGACGCCGCTAGGGCGGAATTGCGCACTGTTCG
                          cagggaacccgctcgcaacgtcacccgatcaacggtcggccgcaacgtcaccctgttcg
                                                                                                                                   GCCTCATGACCAAAAAACGCCGGCCACATCGCCTGGGAAACGGAATGGGTCCACTCAGATC
                                                                                                                                                          accggatcacaaagaacccgctcagcaccgcccatgcgaccctctggggccccgcagacg
                                                                                                                                                                                                    ACATGGCGGCGTGCGCCGAAGGCCTTCGGCGCGCGCGTCGACGGCGACCGCAGTTACTCAG
                                                                                                                                                                                                                             tgctcgcccgcgtcgagcagggcctatgcgacgttctcggcggcgatgcatcctacgggc
                                                                                                                                                                                                                                                                    TGTGGGGACTCAACGCCCTGTTCCACGCACCGAATACGCGGGGGGGTAAGCCGCTCGCAT
                                                                                                                                                                                                                                                                                        totatgccttgaagaaccctgtgtgtctgaccgatgccgcgcggcggcgacggcctatcaacc
                                                                                                                                                                                                                                                                                                                                         GGTCCCATCCGCTGCCCAACGCGATCGTGGGCAATCGCGCCAACGCCACACGCAG
                                                                                                                                                                                                                                                                                                                                                               tgccttcaccgtcctacgtgtccat-----gaaccgtgtcacgaccaccggacacatcg
                                                                                                                                                                                                                                                                                                                                                                                                         ACCTGCTGGTCGTGGACGTAGACCATCCAGACGCAGCGCTCCGAGCGCTCAGCGCCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGCCGCGCGTCGGCCCTAGGGCCCCGGTACATCGAGGGGGAACCGAAGAGGGCCTGGCAA 2735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tgactcggcagagggcgctggagctgccttacatcgaagcgaacccgttggtcatgcagt
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                                                                 TCTACACACTCAGCCACATCGAGGCGGAGCTGGGGGGGGAACATGCCACCGCCGCGCTGGC
                                                                                               cgctctacgagctgcgcgccctcgcacacccctcgacgagatccacgcactgccggagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding strand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68.6; DI Pred. No. 1.3e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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.3e-06;
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ARBSULT 15
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XX W09221
XX WPI; 10-DEC
XX WPI; 17
XX WPI; 17
XX WFI; 10-DEC
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                                                                                                                                                                         This sequence represents that of plasmid pMV101. This is a modi-
version of plasmid pYUB125, which had 792 bases of the tet gene
(inactivated by prior manipulations) deleted. The plasmid
represents an expression vector. The HSP61 coding sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ31743
                                                                     inserted between the NheI and BamHI sites to form pMV65A.

NOTE: when the proteins encoded by this sequence were decoded, the published sequence was found to contain approx. 65 codons which did not code for the amino acids dictated by the universal genetic
                                                                                                                                                                                                                                                                                                             Example 1;
                                                                                                                                                                                                                                                                                                                                                             transformed Mycobacteria
                                                                                                                                                                                                                                                                                                                                                                                      Tetanus vaccination -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEDI-) MEDIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-1991;
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Query Match Best Local Similarity

1.6%; 47.6%;

Score Pred.

58.6; DB 13; No. 0.00032;

Length 4811;

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                                             807 acggtcggcgcaacgtcaccctgttcgacaccacccgcatgtgggcataccggggccgtc 866
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Search completed: October 6, 2002, 16:32:33 Job time: 18386 sec

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Copyright (c) 1993 - 2000 Comp
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ALIGNMENTS

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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr -

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and library colleges the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and library colleges the same strain used for the BDGP's pl and EST libraries.
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BACR19D16 of RPCI-98 library from
fly), genomic survey sequence.
                                                                                                                                                   and how to order individual BAC clones, the entire library, filters for hybridization from the BACPAC Resource Center of found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/clone_lib="RPCI-98"
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                                                                                                        Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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645 bp DNA linear GSS 26-JUL-1:
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN08C07 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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/note="end : TET3"
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/organism="Drosophila
/plasmid="pBeloBAC11"
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/clone_lib="DrosBAC"
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department o Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
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BP 191 91006 EVAL COLOR.

WWW. genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BBGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BBGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Canacias at the Roswell Park Cancer Institute in Buffalo,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic survey sequence.
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61 c 61 g
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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  survey sequence TET3 end of BAC #
rom Drosophila melanogaster (fruit
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                                                                                                          TITLE
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Best Local
                     TITLE
                                                                                                                                        AUTHORS
                                                      AUTHORS
   JOURNAL
                                                                                        JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gcccgtaggagacggtccgggcaccgtcgtacccgtgcgtctcgacgcggccaccgttgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAAASAAASSASSAASVVGAACSSGSGASGSSSAGAARARCASVCASSASSGSCSGCSSS 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1091 bp DNA linear GSS 03-NOV-200 Pan troglodytes DNA, clone: PTB-089D22.R, genomic survey sequence. AG089860 AG089860.1 GI:16641662 GSS; GSS (genome survey serveror.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                     Direct Submission
                                 Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y
                                                                                   Unpublished
                                                                                                      Totoki,Y., Watanabe,H. and Sakak.
BAC end sequences of Library PTB
                                                                                                                                      Fujiyama,A.,
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                          mammaila;
                                                                 (bases 1 to 1091)
                                                                                                                                                          (sites)
                                                                                                                                                                                                          troglodytes
                                                                                                                                                                                                                      GSS (genome survey sequence).
troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
Library clone:PTB-089D22.R.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR10E16"
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                                                                                                                                                                        Eutheria;
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                                                                                                                                    Hattori, M.,
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                                                                                                                                                                        Primates;
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Pred. No. 0.28;
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77 g
                                                                                                                     Toyoda, A.,
nd Sakaki, Y.
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                                                                                                                                                                      Catarrhini;
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                                                   Taylor, T.D.,
                                                                                                                                    Taylor, T.D., Yada, T.,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                              AQ744715

HS_5505_A2_E03_SP6 RPCI-11 Human Male BAC Library Homo genomic clone Plate=1081 Col=6 Row=I, DNA sequence.
Homo sapiens
Eukaryota; M
                                                                  genomic clone
AQ744715
                                                        AQ744715.1
                            human.
                                                                                                                                                                                                             3290
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R.Site 1
R.Site 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Pan troglodytes"
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  Metazoa;
                                                       GI:5522237
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: SacI
: SacI.
Chordata;
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Pred. No. 0.
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Craniata;
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 Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1091;
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1 others
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 Euteleostomi;
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GCCCC 156
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                                                                                                                 cgtgctctacgcggccacccacgttctcaactcccggccactcgacgacgaagacgaccc
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                                                                                                                                                                al Similarity
146; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
http://www.htsc.washington.edu
plate: 1081 row: I column: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 874.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mahairas,G.G., Wallace
Keller,A., Shaker,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High Throughput Sequencing University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 874)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ing the human genome
Natl. Acad. Sci. U. S. A. 96 (17),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI
Male blood DNA was isolated from one randomly chosen
and partially digested with a combination of EcoRI an
EcoRI Methylase. Size selected DNA was cloned into th
pBACe3.6 vector at EcoRI sites"

183 c 412 g 86 t 50 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/clone="plate=1081 Col=6 Row=I"
/clone_lib="RPCI-11 Human Male I
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 53; DB 12;
Pred. No. 1.7;
0; Mismatches 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Male BAC Library'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 874;
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RESULT B96799

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AUTHORS
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DEFINITION
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Best Local Similarity
Matches 187; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
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                   938
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ccacgcactgccggaggcagggaacccgcgtcgcaacgtcacccgatcaacggtcggccg 817
                                                                                                                                                                                                                                                                                                                                                                                                                   gcgacggcctatcaacctgctcgcccgcgtcgagcagggcctatgcgacgttctcggcgg 637
                                                    GACCATCTCACGCGCCATGGTCGGCCGCACCGTCGCCGATGTCGAGCGCGACTTGATCCT
                                                                                                                                          caacgtcaccctgttcgacaccacccgcatgtgggcataccgggccgtccggcactcctg
                                                                                                                                                                                                                                                                                    ctggggccccgcagacgcgctctacgagctgcgcgccctcgcacacaccctcgacgagat 757
                                                                                                                                                                                                                                                                                                                        CAAATACGCCAAGGCCAACGGTCTCGGCCGCCGCGTGCTCTCCGCCGAGGCCCGTGACGC 123
                                                                                                                                                                                                                                                                                                                                                      cgatgcatcctacgggcaccggatcacaaagaacccgctcagcaccgcccatgcgaccct 697
                                                                                                                                                                                                                                                                                                                                                                                     GCTTCCGGCTTTGCGCGAGCGCCCCGGCGATACCGCCGCGCGCTGGCCGAGCACTTCGTCGA 63
                                                                              gggcggcccggtcgccgaatgggagcacaccgtattcgagcacatccacctactgaacga 937
                                                                                                                     CGGCCTCAGCGAGGTCGTCGCCATGGCTTCGGTCGCGACCCAGGCCGCCCAGACCGCCGA
                                                                                                                                                                                     CGTGCTGCTGTCGGGTGGCGAGATCATCGGCCCCGACGCCATCTCGATGCCCGATGGCAC
                                                                                                                                                                                                                                                      CTTGCTCCGCGCCCCGTGGCCCGGCAACGTCCGTGAACTCGAGAACACCCTGCACCGCGC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis Genomi
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l (bases 1 to 570)
1 (bases 1 to 570)
Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K., Golder
Rerry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
B96799
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T32L9TR TAMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other_GSSs: T32L9TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A BAC End Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: rounsley@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eg primer: M13 Reverse
Lass: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medical Center Dr., Rockville,
301 838 0200
301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop:
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="T32L9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="hermaphrodite"
/note="vector: BeloBACII; Site_1:
; Produced by Rod Wing"
; 232 c 163 g 79 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:2998045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="TAMU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 equence Database for Genomic Sequencing.
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Pred. No. 1.9;
0; Mismatches
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thaliana
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                                                                                                                                                    877
                                                                                                                     303
                                                                                                                                                                                   243
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β Q

73

653 gcaccggatcacaaagaacccgctcagcaccgcccatgcgaccctctggggccccgcaga 712

GGACCGCGACAAGAACCACCTGCGGCTGACCTTCCGCGCCACGCTCATGGGGCCAGGCGTG 132

Matches

154;

Conservative

0;

Mismatches

171;

Indels

0

Gaps

0

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RESULT
AW132314
                                                                                                    BASE COUNT
ORIGIN
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JOURNAL
  Best
                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW132314 448 bp mRNA linear EST 30-NOV-2001 se02e02.yl Gm-c1013 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1013-2355 5' similar to TR:077046 077046 AMINOPEPTIDASE N ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: estéwatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
call: (800)-533-4363 or contact via email: ccueresgen.com
seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shoemaker, R., Keim, P., Vo
, A., Bolla, B., Marra, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
AW132314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shoemaker R/Public Soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine.
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  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 401.
                                                                                                                           84
                                                                                                                                                                                                                                          /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from whole seedlings of 2-3 week old greenhouse grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction
                                                                                                                           Erpelding."
                                                                                                                                                                                                  site of the pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      greenhouse
                                                                                                                                                                        was constructed by Dr. Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Glycine max"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Whole seedlings,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="GENOME SYSTEMS CLONE ID:
/clone_lib="Gm-cl013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
1.48;
Score 51.4;
Pred. No. 3;
                                                                                                                           151
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                       DВ
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                       9
                                                                                                                                                                             Shoemaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2-3 week old seedlings,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gm-c1013-2355"
                       Length 448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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National Institutes of Health, Mammalian
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Clone distribution: MCC clone distribution information can
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/clone="IMAGE:5064900"
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/clone_1ib="NCI_CGAP_Kid14"
/lab_host="0H10B (Tl phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. | " a 625 c 311 g 163 t
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNS01087 961 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN03H07 of DrosBAC library from Drosophila melanogaster (fruit
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1 (bases 1 to 961)
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208 c 163
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/clone="BACN03H07"
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1100)
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
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/plasmid="pBeloBAC11"
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/clone="BACN16D22"
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170 c
                                          /clone_lib="RPCI-98"
/clone="BACR14N09"
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/organism="Drosophila
/db_xref="taxon:7227"
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Drosophila melanogaster genome survey sequence T7 end of BAC * BACR14809 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 932)
                                                                                                                                                                                                                                                             Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail : Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                  Direct Submission
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segref@genoscope.cns.fr
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
                                                                                                                                                                                                                                                                                                           AV623353 AV623353 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas reinhardtii cDNA clone LC062e06_r 5', mRNA sequence.
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
                                                                                     Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Nakamura, Y. and Tabata, S.

Generation of expressed sequence tags from low-CO2 and adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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/db_xref="taxon:7227"
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a 202 c 241 g
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Location/Qualifiers
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asamizu@kazusa.or.jp,

URL: http://www.kazusa.or.jp/en/plant/

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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Mracomorpha: Ephydroidea; Drosophilidae; Drosophila.
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as par-
collaboration with the European Drosophila Genome Project (EDM
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                           Submitted (23-JUL-1999) Genoscope - Centre RP 191 91006 EVRY cedex - FRANCE (E-mail:
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                                                                                                                                      Direct Submission
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/clone=lib="chlamydomonas reinhardtii 5% to 0.04% CO2"
/clone=lib="chlamydomonas reinhardtii 5%; Site_1: EcoRI; Site_2:
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The CDNA library was constructed from cells cultured in a carbon stress acclimatized condition in which carbon dioxide concentration in the bubbling gas was changed from 5% to 0.04%"
184 c 146 g 78 t
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/strain="C9"
/db_xref="taxon:3055"
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Pred. No. 4.9;
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survey sequence T7 end of BAC
rom Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
NTTTSSNNSNSSCNTTSANNTSSTNTTNTAGNNNNATSSSNSNNNSSNNNSNNNSNNSSGSG
                                                                                                cctgctcgcccgcgtcgagcagggcctatgcgacgttctcggcggcgatgcatcctacgg
                                                                                                                                                                                                                                                                                                                                                    NNSSSGSSSNNNNSGGSSSNNSNSNNGSGSSSSSSNSNTSSNNNSNNTNSNNNSSNNNNSS
                                                                                                                                                                                                                                                                                                                                                                                     ccggcacgtgactcggcagagggcgctggagctgccttacatcgaagcgaacccgttggt
                                                                                                                                                                                                                                                                                                                                                                                                                         gcaccggatcacaaagaacccgctcagcaccgcccatgcgaccctctgggggccccgcaga
                                                                                                                                      SSSSTTNSTSTSSSSSNSTGSSSSTTTTNSSASSNNNSNNNNGNSSSSNAANSTSTTNSS
                                                                                                                                                                     cgtctatgccttgaagaaccctgtgtgtctgaccgatgccgcgcggcggcgacggcctatcaa
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/plasmid = "pBeloBAC11"
/db_xref = "taxon:7227"
/clone_lib = "DrosBAC"
/clone="BACN08C07"
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26 c 85
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Search Job tim rch completed: October time: 17806 sec 6 2002, 16:22:38

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Result
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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Perfect score:
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length:
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Match
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Gapop 10.0 , Gapext 1.0
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3555
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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-07-977-630-1
US-07-977-630-2
US-07-977-630-2
US-07-977-630-2
US-07-977-630-21
US-08-316-950-15
PCT-US95-12642-15
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US-08-510-6468-3
US-09-231-818-3
US-09-231-818-1
US-09-231-818-1
US-09-320-678-19
US-09-310-537-32
US-09-310-537-32
US-09-320-678-19
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43	43	43	43	43	43.4	43.4	43.8	43.8	43.8	43.8	44.2	44.2	44.4	44.6	46.4	46.4	46.4
1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.3	1.3	1.3	1.3
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US-08-804-227C-7	US-08-402-068-3	US-08-402-066-3	US-08-508-004-3	US-08-402-282-3	US-09-434-288-1	US-09-197-649-7	PCT-US95-09323-1	US-08-476-519-1	PCT-US95-09323-10	US-08-476-519-10	US-08-765-907A-6	US-08-765-907A-14	US-09-105-537-34	US-09-130-114-2	US-08-459-255-1	US-08-459-254-1	US-08-461-179-1
Sequence 7, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 6, Appli	Sequence 14, Appl	Sequence 34, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

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CURRENT APPLICATION.

APPLICATION NUMBER: US/07/977, bid FILING DATE: No. 5583038ember 17, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Herron, Charles J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 469201-174
FELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6407 nucleotides
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                                                                                                                                                                    ; MOLECULE TYPE: nucleic acid US-07-977-630-1
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US-07-977-630-1/c
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                                                                       Query Match
Best Local Similarity 47.1
Matches 274; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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CITY: New Jersey
"TATE: New Jersey
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MEDIUM TYPE: 3.5 inc
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TITLE OF INVENTION: BACTERIAL EXI
TITLE OF INVENTION: DNA ENCODING
NUMBER OF SEQUENCES: 84
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2852 AGCTCTGGCTGCCGTACTGGCCGCTGGCAAGCGACGATCTGCTCGAGGGGATCTACCGCC 2793
                   301 agagctggctgccacgcaagccgctggcgtcagccgagaagtctggggggtaccggcacg 360
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STRANDEDNESS:
TOPOLOGY: cir
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                                                                     Score 82.2; DB Pred. No. 2.1e-0; Mismatches
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2.1e-10;
nes 293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
             TELEFAX: 20
                                                                                                                            OPERATION OPERATE ASCII
SOFTWARE: ASCII
CURRENT APPLICATION NUMBER: US/07/977,630
APPLICATION NUMBER: US/07/977,630
FILING DATE: No. 5583038ember 17,
FILING DATE: No. 5583038ember 17,
                                                      ATTORNEY/AGENT INFORMATION:
NAME: HETTON, Charles J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 46:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2612
SEQUENCE
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                          TELEPHONE:
                                                                                                                                                                                                                          COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                         STREET: 6 Becker CITY: Roseland
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                               COUNTRY:
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CHARACTERISTICS
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                             201-994-1744
                                                                                                                                                                                                                                                                                                              USA
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                                              201-994-1700
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Stewart & Olstein
                 SEQ ID NO:
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RESULT 3
US-07-977-630-20
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                                                                                                                                                                                                                                   Sequence 20, Application Patent No. 5583038 GENERAL INFORMATION: APPLICANT: Stover, Ch
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Best Local Similarity
Matches 274; Conserv
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STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: nucleic acid
07-977-630-2
COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch
                                                STREET: 0 L.
STREET: Noseland
CITY: Roseland
CTATE: New Jersey
TISA
                                                                                                                                                                                                  TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
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                                   COUNTRY: U:
ZIP: 07068
                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTACACACTCAGCCACATCGAGGCCGAGCTCGGCGCGAACATGCCACCGCCGCGCTGGC
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                                                                                                          6 Becker Farm
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                                                                                                                                                                                                Stover, Charles K.
VENTION: BACTERIAL EXPRESSION VECTORS CONTAINING
VENTION: DNA ENCODING SECRETION SIGNALS OF LIPOP
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ilarity 47.8%;
Conservative
                                                                                                                           Carella, Byrne, Ba
Stewart & Olstein
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   diskette
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Pred. No. 2.1e-10;
                                                                                                                                           Bain,
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                                                                                                                                             Gilfillan, Cecchi
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RESUL7
US-07-977-630-21/c
Sequence 21, Application US/07977630
Patent No. 5583038
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Best Local :
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4120 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: nucleic acid
07-977-630-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 460
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                      2682
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ATTORNEY/AGENT INFORMATION:
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Local Similarity 47.6%;
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SOFTWARE: ASCII
                                                                                                                                                     acaccaccgcatgtgggcataccgggccgtcc 867
                                                                                                                                                                                                        GTCAGCAGACCACGTACAAAGCGGCTCCGACGCCCTAGGGCGGAATTGCGCACTGTTCG
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                                                                                                                                                                                                                                   cagggaacccgcgtcgcaacgtcacccgatcaacggtcggccgcaacgtcaccctgttcg 834
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                                                                                                                               ATTCCGTCAGGTTGTGGGCCTATCGTCCCGCCC 2954
                                                                                                                                                                                                                                                                                TCTACACACTCAGCCACATCGAGGCCGAGCTCGGCGCGAACATGCCACCGCCGCGCTGGC
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Pred. No. 4.4e-10;
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Best Local Similarity
Matches 273; Conserv
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FILING DATE: No. 5583038ember
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Herron, Charles J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 4692
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stover, CITITLE OF INVENTION: ITTLE OF INVENTION: ITTLE OF SEQUENCES:
                                                                                                                                                                                                                                      1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: double TOPOLOGY: circular MOLECULE TYPE: nucleic acid 7-977-630-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 4120 nucleotid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
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TCTACACTCAGCCACATCGAGGCCGAGCTCGGCGCAACATGCCACCGCCGCGCTGGC 1260
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                                cgctctacgagctgcgcgccctcgcacacaccctcgacgagatccacgcactgccggagg 774
                                                                           GCCTCATGACCAAAAACCCCGGCCACATCGCCTGGGAAACGGAATGGCTCCACTCAGATC 1320
                                                                                                                                                      ACATGGCGGCGTGCGCCGAAGGCCTTCGGCGCGCCGTCGATGGCGACCGCAGTTACTCAG 1380
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Stewart & Olstein
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BACTERIAL EXP
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Pred. No. 4.4e-10;
0; Mismatches 294;
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                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                Matches 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-903
INFORMATION FOR SEQ ID NO: 11:
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CURRENT APPLICATION NUMBER: US/08/316,950
APPLICATION NUMBER: US/08/316,950
APPLICATION NUMBER: 03-0CT-1994
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: STOVER, Charles APPLICANT: HICKEY, Mark J.
                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                       361 tgactcggcagagggcgctggagctgccttacatcgaagcgaacccgttggtcatgcagt 420
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1..4120
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                               ccttggtcatcaccgatcgagatgcttcggatgctgactgggccgcagacctcgctgggc 480
                                                                   AAAGCCGCGCGTCGGCCCTAGGCCGCCGGTACATCGAGGCGAACCCCAACAGCGCTGGCAA 2501
                                                                                                                                       AGCTCTGGCTGCCGTACTGGCCGCTGGCAAGCGACGATCTGCTCGAGGGGGATCTACCGCC 2441
ACCTGCTGGTCGTGGACGTAGACCATCCAGACGCAGCGCTCCGAGCGCTCAGCGCCCGGG 256:
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                                                                                                                                                                                                              Conservative
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Pred. No. 4.4e-10;
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PCT-US95-12642-11
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                                                                                               TELEFAX: (415) 543-504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12642
                                                                                                                                                                             NAME: HUNTEY, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/316,950 FILING DATE: 03-OCT-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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TITLE OF INVENTION: Mycobacterial Reporter Strains and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2922 ATTCCGTCAGGTTGTGGGCCTATCGTCCCGCCC 2954
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MOLECULE TYPE:
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                                    TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                       TOPOLOGY:
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                                                         nucleic acid
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DNA (plasmid)
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                                                                                                                                                                                                                                                           Sequence 15, Application US/08316950 Patent No. 5679515 GENERAL INFORMATION:
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Best Local
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               TITLE OF INVENTION:
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OTHER INFORMATION:
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Steuart Street Tower, One Market
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No. 4.4e-10;
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Version #1.
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Best Local Similarity 47.6%;
Matches 273; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 4296 base pairs
TYPE: nucleic acid
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 03-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /standard_name=
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                acaccacccgcatgtgggcataccgggccgtcc 867
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ATTCCGTCAGGTTGTGGGCCTATCGTCCCGCCC
                                                                 GTCAGCAGACCACGTACAAAGCGGCTCCGACGCCGCTAGGGCCGAATTGCGCACTGTTCG
                                                                                                cagggaacccgcgtcgcaacgtcacccgatcaacggtcggccgcaacgtcaccctgttcg
                                                                                                                                   TCTACACACTCAGCCACATCGAGGCCGAGCTCGGCGCGAACATGCCACCGCCGCGCTGGC
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Pred. No. 4.5e-10;
0; Mismatches 294;
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RESULT 8
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Sequence 15, Application PC/TUS9512642

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; OTHER INFORMATION:
PCT-US95-12642-15
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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INFORMATION FOR SEQ ID NO:
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NAME/KEY: misc_feature
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08 FILING DATE: 03-OCT-1994 ATTORNEY/AGENT INFORMATION: NAME: Hunter, Tom
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                  GGTCCCATCCGCTGCCCAACGCGATCGTGGGCAATCGCGCCAACGGCCACGCACACGCAG
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Pred. No. 4.5e-10;
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                                                                                                                                                          ; LOCATION: 1..4352
; OTHER INFORMATION: /standard_name=
US-08-316-950-16
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                                                                      Matches
                                                                                       Query Match
Best Local
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
2405
                                                                                                                                                                                                                               MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 4352 base pairs
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NAME: Hunter, Tom
REGISTRATION NUMBER: 38,4
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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              301 agagctggctggccacgcaagccgctggcgtcaggccgagaagtctggggggtaccggcacg 360
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AGCTCTGGCTGCCGTACTGGCCGCTGGCAAGCGATCTGCTCGAGGGGATCTACCGCC 2464
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                                                                                     Similarity
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                                                                   Score 80.6; DB 1;
Pred. No. 4.5e-10;
0; Mismatches 294
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                                                                                                    Length 4352;
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PCT-US95-12642-16

Sequence 16, Application PC/TUS9512642

GENERAL INFORMATION:
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APPLICANT: 201 Elliott Avenue West, Suite
APPLICANT: Seattle, Washington 98119
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                                                                            FILING DATE: 03-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,950
FILING DATE: 03-OCT-1994
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                        STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco
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                                                                                                                                            FILING DATE: 0
CLASSIFICATION:
                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                            APPLICATION NUMBER: PCT/
FILING DATE: 02-OCT-1995
                                                                NAME:
                                                                                                                                                                                                                                                                                                              COUNTRY:
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INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARGTERISTICS:
LENGTH: 4352 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                            Sequence 13, Applicat Patent No. 5679515 GENERAL INFORMATION:
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Best Local Similarity
                             APPLICANT: STOVER, Charles K. APPLICANT: HICKEY, Mark J. TITLE OF INVENTION: Mycobacteri TITLE OF INVENTION: Thereof NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS:
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OTHER INFORMATION: /standard_name- "plasmid
                     ADDRESSEE:
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3: Townsend and Townsend Khourie
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Best Local Similarity
Matches 273; Conserv
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INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 4505 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                              2682
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
2862 GTCAGCAGACCACGTACAAAGCGGCTCCGACGCCGCTAGGGCCGGAATTGCGCACTGTTCG
                                                                       2802 TCTACACACTCAGCCACATCGAGGCCGAGCTCGGCGCGAACATGCCACCGCCGCGCGCTGGC
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                             775 cagggaacccgcgtcgcaacgtcacccgatcaacggtcggccgcaacgtcaccctgttcg 834
                                                                                                        715 cgctctacgagctgcgccctcgcacacaccctcgacgagatccacgcactgccggagg
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OTHER INFORMATION:
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CLASSIFICATION:
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)N: 435
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Pred. No. 4.6e-10;
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                                                                                                                                                                                                                                                                                                Query Match
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 4505 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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FILING DATE: 03-OCT-1994
ATTORNEY/BAGENT INFORMATION:
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PRIOR APPLICATION DATA:
US 08/316,950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                      2502 ACCTGCTGGTCGTGGACGTAGACCATCCAGACGCAGCGCTCCGAGCGCTCAGCGCCCGGG 2561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Mycobac TiTLE OF INVENTION: Thereof
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                                                                                                              2442 AAAGCCGCGCCGTCGGCCCTAGGCCGCCGGTACATCGAGGCGAACCCAACAGCGCTGGCAA 2501
                                                                                                                                                                                    2382 AGCTCTGGCTGCCGTACTGGCCGCTGGCAAGCGACGATCTGCTCGAGGGGATCTACCGCC 2441
                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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OPERATING SYSTEM: PC-DOS ~~
SOFTWARE: Pater
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LOCATION: 1.4505
OTHER INFORMATION:
                                                                                                                                                                                                                                                            Local Similarity
mes 273; Conserv
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/
FILING DATE: 02-OCT-1995
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VENTION: Mycobacterial Reporter Strains and
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euart Street Tower, One Market Plaza
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Pred. No. 4.6e-10;
0; Mismatches 294;
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US-08-316-950-12
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US-08-316-950-12
                                                                                                                                                REFERENCE/DOCKET NUMBER: 1537
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 6047 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08316950 Patent No. 5679515 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08,
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
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MEDIUM TYPE: Floppy disk
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                                                                   FEATURE:
                                                                                      MOLECULE TYPE:
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            NAME/KEY: misc_fea
LOCATION: 1..6047
OTHER INFORMATION:
                                                                                                      STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                               NAME: Hunter, Tom REGISTRATION NUMBER:
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Mark J.
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                "plasmid pMH30-lux"
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PCT-US95-12642-12
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Best Local Similarity 47.6%;
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          APPLICANT: PathoGenesis Corporation
APPLICANT: 201 Elliott Avenue West,
APPLICANT: Seattle, Washington 98119
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                                                                                                                                                                                                               STREET: Steuart Street Tower, One CITY: San Francisco
CLASSIFICATION:
                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                       ADDRESSEE:
                  FILING DATE:
                                 APPLICATION NUMBER:
                                                                                                                                                                             COUNTRY:
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euart Street Tower, One Market Plaza
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Pred. No. 5e-10;
"" wiscmatches 294;
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RESULT 15
US-08-316-950-17
; Sequence 17, Application US/08316950
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Best Local Similarity
Matches 273; Conserv
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TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 12:
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NAME/KEY: misc_feature
LOCATION: 1.6047
LOCATION: /st;
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LENGTH: 6047 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER: US 0:
FILING DATE: 03-OCT-1994
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
                                                                                                                        2945 ATTCCGTCAGGTTGTGGGCCTATCGTCCCGCCC 2977
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REGISTRATION NUMBER: 38,498
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Pred. No. 5e-10;
0; Mismatches 2
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INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 6171 base pairs
TYPE: nucleic acid
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APPLICANT: HICKEY, N
TITLE OF INVENTION:
TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                          2682 ACATGGCGCGTGCGCCGAAGGCCTTCGGCGCGCCGTCGATGGCGACCGCAGTTACTCAG 2741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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OPERATING SYSTEM:
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STATE: California
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OTHER INFORMATION: /standard_name=
OTHER INFORMATION: pMV261-lux"
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TOPOLOGY: 11r
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Local Similarity 47.6%;
ses 273; Conservative
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accggatcacaaagaacccgctcagcaccgcccatgcgaccctctggggccccgcagacg 714
                                                                      tgctcgcccgcgtcgagcaggcctatgcgacgttctcggcggcgatgcatcctacgggc 654
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Steuart Street Tower, One Market Plaza
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SYSTEM: PC-DOS/MS-DOS
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ALIGNMENTS

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AAY44636 standard; Protein; 303 AA

(first entry) ans 250 かずる traction

ANY44636
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XX O7-A
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XX C Propionibacterium LMG 16545; vector; plasmid; antigen; vaccine; enzyme; nutritional factor; growth factor; clotting factor; antimicrobial; drug hormone; vitamin B12; animal feed; lactic acid bacteria; foodstuff; 07-APR-2000 AAY44636; Propionibacterium LMG 16545 protein-1. 252

drug;

Propionibacterium freudenreichii LMG 16545

WO9967356-A2

29-DEC-1999.

25-JUN-1999; 99WO-EP04416

25-JUN-1998; 98EP-0305033

(KONN) GIST-BROCADES BV.

Pouwels PH, Van Luijk N, Jore JPM, Luiten

WPI; 2000-136977/12. N-PSDB; AAZ49691.

Novel vectors containing Propionibacterium sequences, used to homologous or heterologous proteins $\,$ express

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  17-NOV-1992;
21-OCT-1991;
                                                                                                                                                                                                                                                                                                                                            Plasmid pMV101; Mycobacteria; lipoprotein secretion signal sequence; antigen; bacterial vaccine; Lyme disease; Borrelia burgdorferi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW14835 standard; Protein;
                                                                                     21-OCT-1991;
                                                                                                                                          10-DEC-1996
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AAR20992 ID AAR2

AAR20992 standard; Protein;

368

03-JUN-1992

(first entry)

Polymerase chain resistance; BCG;

reaction; mycobacterial promoter; Bacille Calmette-Guerin; origin of

origin of

Protein "e" encoded by mycobacterial plasmid pMV101.

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacteria expressing secretion signal of lipoprotein and heterologous antigen, esp. outer surface protein A or B of Borrelia burgdorferi - are used in the form of a live bacterial vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-042315/04.
N-PSDB; AAT64413.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 DSFETLFPESWLPRKPLASAE-KSGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASD
w
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taastvarra
                                                                                       GIASGASRRA
                                                                                                                                               GPLGLNELKHLSRSISRW-----VWRN---FTPETFRARQKAISLRGASKGGKEGGHKG
                                                                                                                                                                                                                                                                                                         VLGGDASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAGNPRRNVT--
                                                                                                                                                                                                                                                                                                                                                                ADWAADLA--GLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCD 118
                                                                                                                                                                                                                                                                                                                                                                                                                 defeql----wlpywplasddllegiyrq-srasalgrryieanptalanllwydydhpd 120
                                                                                                                         gplpdsevraiansiwrwittksriwadgivvyeatlsarqsaisrkgaa-----
                                                                                                                                                                                                 aaptplgrncalfdsvrlwayrpalmriylptrnvdglgraiyaecharnaefpcndvcp
                                                                                                                                                                                                                                     --RSTVGRNVTLFDTTRMWAYRAVRHSWGGPVAEWE---HTVFEHIHLLNETIIADEFAT 231
                                                                                                                                                                                                                                                                     avdgdrsysglmtknpghiawetewlhsd----lytlshieaelganmppprwrqqttyk
                                                                                                                                                                                                                                                                                                                                             aalralsargshplpnaivgnranghahavwalnapvprteyarrkplaymaacaeglrr 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                    358
                                                                                       292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 329; DB 18;
Pred. No. 6.8e-26;
9; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid pYUB12 was constructed by ligating a 5kb Sau3 fragment from CD pAL5000 (contg. a replication origin from M.fortuitum) to BamHI-CD dispested pIJ666 (contg. an E.coli ori and kanamycin-neomycin resistance sequences). A 2586bp HpaI-EcoRV fragment from pYUB12 (comprising the minimum sequence necessary for plasmid replication in BCG) was ligated to PvuII-digested pYUB8 to form pYUB53. (Plasmid CV pYUB8 is a pBR322 deriv, which includes an E.coli replicon and a kanamycin resistance gene). Twelve restriction sites were removed by digesting pYUB53 with Aatl, EcoRV and PstI. To eliminate 792 chases of the (lnactivated) tet gene, the plasmid was digested with CC warI and the 6407bp gel purified fragment was religated/CC valuarised. The resulting plasmid was designated pWI01. The nucleotide sequence of plasmid pWI01 is printed in the specification but the copy quality is too poor to allow the sequence to be included on the GENESEQ nucleotide database. Three proteins are encoded by pWVI01, i.e. the kanamycin resistance protein and proteins "d" and "e" encoded by the complementary are also AAR20991 and AAR20993.
                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA site-specific integration into Mycobacteria - useful as adjuvant in vaccines and as therapeutic agent for malaria, influenza, herpes and human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 24; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09201783-A.
 347
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                                                                                                                                                                                                              119
                              280
                                                          294
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                                                                                                                     234
                                                                                                                                                   173
                                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                        66
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                  DSFETLFPESWLPRKPLASAE-KSGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASD
                                                                            FATGPLGLNELKHLSRSISRW-----VWRN---FTPETFRARQKAISLRGASKGGKEGG
                                                                                                                                                                            avdgdrsysglmtkwpgeiawetewlhsd----lytlshieaelganmpp---prwrqqt 233
                                                                                                                                                                                              VLGGDASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEIHA-LPEAGNPR-----
                                                                                                                                                                                                                                        aalralsargshplpnaivgnranghahavwalnapvprteyarrkplaymaacaeglrr
                                                                                                                                                                                                                                                        ADWAADLA--GLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCD
                              HKGGIASGASRRA
                                                          vcpgplpdsevraiansiwrwittksriwadgivvyeatlsarqsaisrkgaa------
                                                                                                                   tynaaptplgrncalfdsvrlwayrpalmriylptrnvdglgraiyaecrarnaefpcnd
                                                                                                                                                -RNVTRSTVGRNVTLFDTTRMWAYRAVRHSWGGPVAEWE---HTVFEHIHLLNETIIADE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIV OF PITTSBURGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                             368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hatfull G;
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90US-0553907
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                              292
 358
                                                                                                                                                                                                                                                                                                                                                                               19.7%;
                                                                                                                                                                                                                                                                                                                                                                   39;
                                                                                                                                                                                                                                                                                                                                                               Score 315; DB 1
Pred. No. 2e-24;
9; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                    DB 13;
                                                                                                                                                                                                                                                                                                                                                                   128;
                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                          180
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AAR34543
ID AAR3
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                                                                                                                                                                                                                                         This sequence is the tet d gene product encoded by plasmid pMV101. When the nucleotide was decoded, the sequence in the specification was found to contain several deletions and insertions which upset the reading frame. Also many codons were found to encode amino acids contrary to the universal genetic code. In addition two amino acids in the sequence in the specification were given as X and were further defined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytotoxic T-lymphocyte response; transformed Mycobacteria; Mycobacterium smegmatis; vaccine; cell mediated immunity; I
                                                                                                                                                                                                                                                                                                                                                                     Expression vector for expressing protein or polypeptide in mycobacterium - conty DNA sequences encoding ipoprotein secretion signal and peptide heterologous to bacteria expressing fusion protein of lipoprotein heterologous to bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tet d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR34543 standard; Protein;
                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 5; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-APR-1993.
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  181
                          119
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1993-152187/18.
DB; AAQ41316.
                     VLGGDASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAGNP----RRN
                                                                                                defeq1---wlpywplasddllegiyrq-srasalgrryieamptalanllvvdvdnpd
v-dgdrsysglmtkmpghiawetew-----lhedlytlseieaelgawmppprwrqq
                                                 aalralsargsnp
                                                              ADWAADLA--GLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCD 118
                                                                                                                          DSFETLFPESWLPRKPLASAE-KSGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product
                                                                                                                                                                                                                   367 AA;
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91US-0780261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92WO-US09075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                 lpnaivgnrangnaeavwalnapvprteyarrkplatmaacaeglrr 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   influenza virus; CTL;
                                                                                                                                                               18.0%; Score 287.5; DB 14; 33.3%; Pred. No. 1.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "X undefined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pMV101 - a deletion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         undefined
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                                                                                                                                                      Mismatches 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   herpes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutant of pYUB125
                                                                                                                                                      Indels
                                                                                                                                                                           Length
                                                                                                                                                                             367;
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                                                                                                                                                  Gaps
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RESULT
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                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                    Method of inducing cytotoxic T-lymphocyte response - esp. expression products of transformed Mycobacterium are useful as vaccines against HIV, pertussis, malaria, influenza virus, herpes
                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                 This sequence is the tet d gene encoded by plasmid pMV101
                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 5; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytotoxic T-lymphocyte response; transformed Mycobacteria; Mycobacterium smegmatis; vaccine; cell_mediated immunity; !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tet d gene product from pMV101 - a deletion mutant of pYUB125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ31727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-433380/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dela Cruz V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pertussis; malaria;
185 raiawsiwrwittxsriwadgivvyeatlsarqsaisrkgaa 226
                             240
                                                       125
                                                                                  183
                                                                                                                                        131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 dvcpgplpdsevraiawsiwrwittxsriwadgivvyeatlsarqsaisrkgaa
                                                                                                             73
                                                                                                                                                                13
                                                                                                                                                                            71 PSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYGHRI 130
                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G
                         KHLSRSISRW-----VWRN---FTPETFRARQKAISLRGAS
                                                    ncalfdsvrlwayrpalmriylptrxvdglgraiyaecrarnaefpcndvcpgplpdsev 184
                                                                                                       tkmpghlawetew-----lhedlytlseleaelgawmppprwrqqttykaaptplgr 124
                                                                                                                                     TKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAGNP----RRNVT----RSTVGR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \verb|tty| kaaptplgrnca| fdsvrlwayrpalmriylptrxvdglgraiyaecrarnaefpcn|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VT----RSTVGRNVTLEDTTRMWAYRAVRHSWGGPVAEWE---HTVFEHIHLLNETIIAD
                                                                               NVTLFDTTRMWAYRAVRHSWGGPVAEWE---HTVFEHIHLLNETIIADEFATGPLGLNEL 239
                                                                                                                                                             plpnalvgnrangnaeavwalnapvprteyarrkplatmaacaeglrravdgdrsysglm 72
                                                                                                                                                                                                                                                                                         248
                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stover CK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92WO-US04538
                                                                                                                                                                                                                  13.7%; Score 218; DB 13; 30.6%; Pred. No. 1.9e-14; ative 30; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             influenza virus; CTL; herpes virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                           272
                                                                                                                                                                                                                                               Length 248;
                                                                                                                                                                                                                     Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272
                                                                                                                                                                                                                    Gaps
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ARESULT ARAS7872 ID AARS AC AARS AC AARS AC CYC KW MYCC KW MYCC KW MYCC XX MYCC XX MO92 XX MO9
AAB35246
ID AAB3
XX
AC AAB3
XX
DT 08-M
DT 08-M
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DE COTY
XX
KW Plas
KW high
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                                                                                                                                                                                                                                                                                                             RESULT
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetanus vaccination - by transformed Mycobacteria
                                                                                                                                        08-MAY-2001
                                                                                                                                                                                                 AAB35246;
                                                                                                                                                                                                                                                      AAB35246 standard; Protein; 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is the tet d gene encoded by plasmid pMV101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-433378/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytotoxic T-lymphocyte response; transformed Mycobacteria; BCG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tet d gene product from pMV101 - a deletion mutant of pYUB125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUN-1993
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                                                                              Corynebacterium thermoaminogenes plasmid pYM4 rep protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 5; 86pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                           185 raiawsiwrwittxsriwadgivvyeatlsarqsaisrkgaa
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Pred. No. 1.9e-14;
0; Mismatches 96;
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6

high temperature

Plasmid; pYM4; rep; coryneform bacterium; L-amino acid; thermostable;

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ARBSULT
AAB35243
JID SAB3
JID SAB3
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XX AAB3
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Best Local S
Matches 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsuzaki Y,
Sugimoto S;
                   Plasmid; pYM1; rep; high temperature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium
                                                                             08-MAY-2001
                                                                                                   AAB35243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5;
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Corynebacterium
                                                      Corynebacterium
                                                                                                                        AAB35243 standard; Protein; 492
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                                                                                                                                                                                                                                                                                                                                       KNPLSTAH---ATLW----GPADALYELRALAHTL-----DEIHALPEAGNPRRNVTR 177
                                                                                                                                                                                                                                                                                                                                                                                  SPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYGHRIT 131
                                                                                                                                                                             --qptvsarstqtqssrgrkalatmgrrgaatsnarrwadpesdyarqtrerlarams
                                                                                                                                                                                                   ARQKAISLRGASKGGKEG-----GHKGGIASGASRRA-----HTRQOFLEGLS
                                                                                                                                                                                                                        agerlkdtkiidayeraynvaqavgadgrepdlpamrdrqtlarrvrayvakg-----
                                                                                                                                                                                                                                              --HLLNETIIADEF-----ATGPLG-----LNELKHLSRSISRWVWRNFTPETFR 260
                                                                                                                                                                                                                                                                   kataeakalaaldatlptaleasgdlidgvrvlwaaegraar-detafrhaltvgyqlka
                                                                                                                                                                                                                                                                                          STV--GRNVTLEDTTRMWAYRA-----VRHSWG--GPVAEWEHTVFEHI------
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                                                                           (first entry)
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thermoaminogenes
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                               coryneform
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                                                                                                                                                                                                                                                                                                                                                                                                          42;
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Pred. No. 0.026;
2; Mismatches 1
                                 bacterium;
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                                                    pYM1 rep protein.
                                 L-amino
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                                acid; thermostable;
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Best Local
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WO200171042-A2
                                                                                                 26-MAR-2002
                                                                                                                       ABB69873;
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Drosophila melanogaster
                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                       ABB69873 standard;
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N-PSDB; AAF24439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 --qptvsarstqtqssrgrkalatmgrrggqk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STV--GRNVTLFDTTRMWAYRA-----VRHSWG--GPVAEWEHTVFEHI-----
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55; Conserv
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                                                                                                            biology;
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; Pred. No. 0.26;
42; Mismatches
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                                                                                                        signalling;
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                                                                Plasmid;
                                                                                       Corynebacterium thermoaminogenes plasmid pYM3 rep protein.
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11-JUL-2000; 2000US-0614150
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                                                             acid; thermostable;
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EP1076094-A2

EP1076094-A2

Corynebacterium

thermoaminogenes

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New plasmids derived from Corynebacterium thermoaminogenes, improving coryneform bacteria, which can grow at elevated to and for producing useful substances (e.g. L-amino acids) -
                                                                 Plasmid; pYM2; rehigh temperature
                                                                                                    Corynebacterium thermoaminogenes plasmid pYM2 rep
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Sugimoto S;
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                                                                        Corynebacterium
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                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                             -HLLNETIIADEF-----ATGPLG-----LNELKHLSRSISRWVWRNFTPET
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                                                                                                                                                                                                                                                                      -qptvsarstqtqssrgrkalatmgrrggqk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                               synthesis.
  2000EP-0127688
                                                                                                                                                           (first
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                                                                        glutamicum
                                                                                                                                                                                                           Protein;
                                                                                                                                                           entry)
                                                                                                                                   fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.0%; Score 95.5;
21.2%; Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                            acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                           610
                                                                                                                                   SEQ ID NO:
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.42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         improving
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DВ

22;

Length

16;

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16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                                              mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                          Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                              The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. I are useful for identifying the mutation point of a gene derived from
Sequence
                                   European Patent Office.
                                                                                                                                                                                                                                                                                     Claim 17; SEQ ID NO: 4495; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KYOW ) KYOWA HAKKO KOGYO
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 610
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; 2000JP-0159162.
; 2000JP-0280988.
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Senoh A, Ik
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ID AAE1
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AC AAE1
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Best Local Similarity
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                           AAE10136;
                                                          AAE10136 standard;
29-NOV-2001
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                                                                                                                                wpaellgyagkgsrggeigdl
                                                                                                                                                             KAISLRGASKGGKEGGHKGGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGAYRHVTRQRALELPYIEANPLVMQS----LVITD-RDASDADWAADLAGLPSPSYVSM 78
                                                                                                                                                                                                                        ADEFATGPLGLNELKHLSRSISRWVWRNFTPE-----
                                                                                                                                                                                                                                                    kgredwrpnvlkfslnllddirp---ramsrdidwgipipvegwqdnnakklyvwfdavv
                                                                                                                                                                                                                                                                                                             gargdqcdncgnqldpadlinpvskingetpefvetehflldlpalaea-----ltewl
                                                                                                                                                                                                                                                                                                                                           ASYGHRITKNPLSTAHATLWGPADALY----ELRALAHTLDEIHALPEAGNPRRNVTRST
                                                                                                                                                                                                                                                                                                                                                                     trtttsnhyavvqelfrglydngymikettlgaispstgr---tlpdryiegtcpicgtd
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(first entry)
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                                                                                                                                                                                                                                                                                -NVTLFDTTRMWAYRAVRH--SWG--GPVAEWEHTVFEHIHLLNETII 225
                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.68;
                                                                                                                                                                                                                                                                                                                                                                                                    ----YALKNPV--CLTDAARRRPINLLARVEQGLCDVLGGD
                                                                                                                                                             284
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Pred. No. 2
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Best Local
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10-APR-2000;
14-APR-2000;
                                                                                                                                                                                                                                                                                                                  The present invention relates to the cloning and sequencing of the cluster encoding a modular type I polyketide synthase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antifungal antibiotics. The present sequence is a transcriptional activator encoding Streptomyces nours nystatin gene, ORF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polyketide synthase; PK antifungal; antibiotic;
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(SNTF )
(ALPH-)
(SINV-)
(DZIE/)
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                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 179; 266pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         New nystatin polyketide synthase polynucleotides useful as antibiotics and antifungals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-FEB-2001;
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                                                                                                                                                                                                             KPLASAEKSGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASDADWAA--DLAGLPSP
isrhnlhlvawvrslddagrfevrlaeraadltvteravalwhmkhgghlldeegyrvgv
                          ISR----
                                                aadmlha--
                                                                                                                                                               SYVSMNRVTTTG-HIVYALKNPVCLTDAARRR----PINLLARVEQGLCDVLG--GDASYG 127
                                                                                                                                                                                      ralaaaphvvalshvtgdrdlqlnvmardpamlsrwvthdlaaldgvraarthlag-pvh 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-557614/62.
DB; AAD17184.
                                                                   DTTRMWAYRAVRHSWGGPVAEWEHTVFEHIHLLNETIIA--DEFATGPLGLNELKHLSRS
                                                                                                                 HRITKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAGNPRRNVTRSTVGRNVTLF
                                                                                                                                        tegsrwrlralgrhqvarl----aadasrhrtdtpafvldeldgqlvtalsvdgraty-
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                                                                                                                                                                                                                                      1 Similarity
79; Conserv
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SEKUROVA O N.
FJAERVIK E.
BRAUTASET T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SB, Sekurova O
, Ellingsen TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SINVENT AS.
DZIEGLEWSKA H.
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2000GB-0008786.
2000GB-0009387.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ON,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sletta
                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fjaervik E, Brautaset
letta H, Gulliksen O;
                                                                                                                                                                                                                                              Score 89; DB:
Pred. No. 1.3;
                                                                                            -rala---eqcgagpd--tvrrrvqr-----lf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene,
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                        ·QKAISLRGASKGG---KEGGHKGGI
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RESULT 1
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Best Local
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                                                                                                                                                                                                                                                                capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryctes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                       The
                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB70548 standard; Protein; 838
                                                                                                                                                                                                                                   specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila;
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 494
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                                                                                                                                                    Local
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scification, but was obtained in electronic i
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                4 FETLFPESWLPRKPLASAEKSGAYRHVTRQRALELPYIE----
                                                                                                                                                                                                                                                                                                                                     invention relates to an
vvpvprptfapeppldvvettasthhlwtevpttaapffteypaevlitthrtsagrftt
                      RRPINLLARVEQGLCDVLGGDASYGHRITKNPLSTAHATLWGPADALYE-------
                                                                   PLYMOSLVITOR-DASDADWAADLAGLPSPSYVS-MNRVTTTGHIVYALKNPVCLTDAAR 102
                                                                                        fttlpp---lpgkpqtsassessgevvtseeyttvphfevsgsksesgseevttvrptaa 433
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                                           {\tt psitisvditssgssssssesvevfttpapvfvqrvttletsisidyvtptplpetttpr}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n,
                                                                                                                                        64;
                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                ABL14651.
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                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   developmental
                                                                                                                                        Conservative
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PWD,
                                                                                                                                                                                                                                                                                                                                                                                             detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biology;
                                                                                                                                        29;
                                                                                                                                       Score 89; DB 1
Pred. No. 4.5;
29; Mismatches
                                                                                                                                                                                                                                                                                                                                    isolated nucleic acid detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers
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                                                                                                                                                              22;
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                                                                                                                                                                                                                                 format
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                                                                                                                                                            Length 838;
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and c
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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC for identifying expressed genes. (I) is useful in gene therapy techniques (CC for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed septification, but was obtained in electronic format directly from WIPO at terminaries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodyversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 59755; 103pp; English
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N-PSDB; AAS93583.
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23-AUG-2000;
                                  at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #29387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 АВG29396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG29396 standard; Protein; 905 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    food supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hhhphheaegttlqpleedeh--hhhhh-----hdeftt 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LRALAHTLDEIHALPEAGNPRRNVT-----RSTVGRNVTLFDTTRMWA
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2000US-0649167.
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Sequence

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  376
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                                                      326
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                                                                                                                                                                                                            171 frynnrerlinkmcgtlpyvapellkrrefhaepvdvwscgivltamlagelpw-----d 225
                                                                                                                                                             226 qpsdscqeysdwkekkt-----ylnpwkkidsa--
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                                                                                                                                                                                                                                         27 YRHVTRQRALE-----LPYI-----EANPLYMQS--LVITDRDASDADWAADLAG 69
                                                                                                                                                                                                                                                                                  Local
                                                                                                      dhqtsvqqlpgeffslenpsdaealyetssglntlse-hgssehgsskhtvaehtsge--
qpsdeqpsgehgsge 390
                           --ADEFATGPLGLNE 238
                                                                                                                                 GHRITKNPLSTAHATLWGPAD--ALYELRALAHTLDEIHALPEAGNPRRNVTRSTVGRNV 184
                                                                                                                                                                                       LPSPS---YVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASY 126
                                                                               TLFDTTRMWAYRAVRHSWGGPV----AEWEHTVFEH-----IHLLNETII-----
                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                     Conservative
                                                   -haesehasgepaatehaegehtvgeqpsgeqpsgehlsgeqplselesge 375
                                                                                                                                                                                                                                                                                  5.5%;
                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                             Score 88;
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7; Mismatches
                                                                                                                                                                                                                                                                                6.4;
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                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                           -plgtssqpne----lsg--si 268
                                                                                                                                                                                                                                                                       87;
                                                                                                                                                                                                                                                                                              Length 905;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                       78;
                                                                                                                                                                                                                                                                  Gaps
                                                                               225
                                                                                                        325
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Search completed: October 4, 2002, 15:34:40 Job time: 93 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
```

OM protein protein search, using sw model

October 4, 2002, 15:33:08; Search time 28.21 Seconds (without alignments) 1032.083 Million cell upd

cell updates/sec

Title: Perfect score: US-09-720-583A-2 1596

1 MDSFETLFPESWLPRKPLAS....IASGASRRAHTRQQFLEGLS 303

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum Maximum BB BB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

score g No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	1	No.	Result
84	84.5	84.5	84.5	84.5	85	85	85	85	85.5	85.5	86	86	86.5	87	87	87.5	•	89	89	89.5	93.5	97.5	98	100	198.5	282.5	282.5	329	Score	
υ ω	5. ₃	5.3	5.3	5.3	5.3	5. ₃	5.3	5.3	5.4	5.4	5.4	5.4	5.4	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.9	6.1	6.1	6.3	12.4	17.7	17.7	20.6	Match	Query
686	4302	500	355	355	900	409	356	356	1366	1217	672	672	497	487	457	409	303	4558	1216	606	228	1876	1461	99	248	304	297	336	Length	
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C90948	A38971	T36090	AE3008	н98275	JH0157	T06767	AE2978	H98304	T35985	T00270	T03457	JC4637	T14609	S60675	S03321	T14611	T36509	C82199	T09224	T37217	н72703	E97944	B70588	S32700	S32701	S04456	S04455	JS0052	ID	
proteinase II [imp	polycystic kidney	probable integral	monooxygenase [imp	ein (cellulase (EC 3.2.	probable transcrip	alkanesulfonate mo	fmnh2-dependent al	probable large Pro	~		transketolase (EC	alanine transamina	hypothetical prote	regulatory protein	alanine transamina	probable molybdopt	RTX toxin RtxA VC1	spindle assembly c		probable translati	zinc metalloprotei	~				1	n - My	Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
82	82.5	82.5	82.5	83	83	83	83	83	83.5	83.5	83.5	83.5	83.5	84	84
5.1	5.2	5.2	5.2	5 .2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.3	5.3
497	1116	1116	814	686	639	559	285	251	1822	1815	863	450	450	1693	686
N	N	N	L	-	N	N	N	N	N	N	<u> </u>	N	N	N	N
T47715	AC2921	D97695	GNMSIP	E64946	D82809	G83024	177964	157999	F87203	S73021	GNHYIH	E98122	E95257	AC3240	G85796
hypothetical prote	cobalamin biosynth	cobN protein homol	retrovirus-related	oligopeptidase B (exodeoxyribonuclea	probable acetolact	SP-10 - western ba	SP-10 - western ba	polyketide synthas	polyketide synthas	retrovirus-related	replicative DNA he	ъ	helicase, SNF2 fam	proteinase II [imp

ALIGNMENTS

37K protein - Mycobacterium fortuitum plasmid pAL5000 C;Species: Mycobacterium fortuitum C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 10-Dec-1999

C; Accession: JS0052;

R;Rauzier, J.; Moniz-Pereira, J.; Gicquel-Sanzey, B. Gene 71, 315-221, 1988
A;Title: Complete nucleotide sequence of pAL5000, a plasmid A;Reference number: JS0052; MUID:89138007
A;Accession: JS0052

from

Mycobacterium fortui

A; Molecule type: DNA A; Residues: 1-336 < RAU>

A;Note: the authors translated the initiation codon GTG f. A;Note: the authors translated the codon ACA for residue R;Labidi, A.; Mardis, E.; Roe, B.A.; Wallace Jr., R.J. Plasmid 27, 130-140, 1992
A;Title: Cloning and DNA sequence of the Mycobacterium fo A;Reference number: JQ1440; MUID:92311251 for e 18

fortuitum

var fortuitum plasmi

residue as Trp

as

A; Molecule type: DNA A; Residues: 160-336 <LAB>

A;Cross-references: GB:M60875; NID:g149984; PIDN:AAA25372.1; PID:g149985 A;Experimental source: var. fortuitum

C; Genetics:

A; Genome: plasmid

C; Function: A; Start codon: GTG

A; Description: this protein is involved in the initiation of plasmid replication C; Superfamily: Mycobacterium hypothetical 37K protein

Š 밁 δÃ 밁 S Matches 104; Query Match 20.6%; Best Local Similarity 33.5%; 119 VLGGDASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAGNPRRNVT-- 176 9 61 ADWAADLA--GLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCD 118 34 DEFEQL----WLPYWPLASDDLLEGIYRQ-SRASALGRRYIEANPTALANLLYVDVDHPD 2 DSFETLFPESWLPRKPLASAE-KSGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASD AALRALSARGSHPLPNAIVGNRANGHAHAVWALNAPVPRTEYARRKPLAYMAACAEGLRR 148 Conservative 39; Score 329; DB 2; I Pred. No. 5e-20; 9; Mismatches 131; Length 336; Indels 36; Gaps 88 60 10;

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149

177 --RSTVGRNVTLFDTTRMWAYRAVRHSWGGPVAEWE---HTVFEHIHLLNETIIADEFAT 231

--LYTLSHIEAELGANMPPPRWRQQTTYK 204

205 AAPTPLGRNCALFDSVRLWAYRPALMRIYLPTRNVDGLGRAIYAECHARNAEFPCNDVCP 264

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RESULT
S04456
S04456
S04456
S04456
A; Solverichia coli plasmid ColE3
C; Species: Escherichia coli
C; Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text,
C; Accession: S04456
R; Yasueda, H; Horii, T; Itoh, T.
Mol. Gen. Genet. 215, 209-216, 1989
A; Title: Structural and functional organization of ColE2
A; Reference number: S04455; MUID:89218922
A; Accession: S04456
A; Status: not compared with conceptual translation
A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-297 < YAS>
C; Genetics:
A; Genome: plasmid
C; Superfamily: Mycobacterium hypothetical 37K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein - Escherichia coli plasmid C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 04-Dec-1992 #sequence_revision 04-Dec-19 C;Accession: S04455 #S:Yasueda, H.; Horil, T.; Itoh, T. Mol. Gen. Genet. 215, 209-216, 1989 A;Title: Structural and functional organization A;Reference number: S04455; MOID: 89218922 A;Accession: S04455
                                      A; Molecule type: DNA
A; Residues: 1-304 < YAS>
A; Cross-references: GB:D30055;
C; Genetics:
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Best Loc
Matches
Superfamily: Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                          KYTHRKFSPEGFSAVQAARGRKGGTKSKRAAVPTSARSLKPWEALGISRATYYRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVRKWAYRAIRQGW---PVFSQWLDAVIQRVEMYNASLPV-----PLSPAECRAIGKSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTRMWAYRAVRHSWGGPV-AEWEHTVFEHIHLLNETIIADEFATGPLGLNELKHLSRSIS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKNPLSTAHATLWGPADALYELRALAHTLDEI-HALPEAGNPRRNVTRS-TVGRNVTLFD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPNITVKNPRNGHAHLLYALALPVRTAPDASASALRYAAAIERALCEKLGADVNYSGLI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPRKPLASAEKSGAYRHVTRQRALELPYIEAN-PLVMQSLVI-TDRDASDADWAADLAGL 70
                      plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                 RWVWRNETPETERARQKAISLRGASKGGKEG-----GHKGGTASGASRRAHTRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CKNP---CH----PEWQEVEWREEPYTLDELADYLDLSASARRSVDKNYGLGRNYHLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYGHRI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPHKPYCTNDFAYGVRILPKNIAILARFIQQNQPHALYWLPFDVDRTGASIDWSD--RNC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPLGLNELKHLSRSISRW-----VWRN---FTPETFRARQKAISLRGASKGGKEGGHKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conceptual translation
hypothetical 37K protein
                                                          NID: 9487267; PIDN: BAA06293.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 282.5;
Pred. No. 3.4e
19; Mismatches
                                                                                                                                                                                                                                                       04-Dec-1992 #text_change
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                                                      PID: g808865
                                                                                                                                                                            ColE3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Shi, SL; Wang, Z.X.; Deng, I.; "...", Spanning of a plasmid pXZ10142 from Corynebacteriu A;Pescription: Complete nucleotide sequence of a plasmid pXZ10142 from Corynebacteriu A:Reference number: S32699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein 3 - Corynebacterium glutamicum
C;Species: Corynebacterium glutamicum
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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S32701
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A; Residues: 1-248 <SHI>
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R; Shi, S.L.; Wang,
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Best Local
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                               276
                                                               177
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228
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                                                                                                                                                                                                                                                                                    73 PSYVSMNRVTTT-----
                                                                                                                                                                                                                                                        N
                                                                                                                       KEGGHKGG
                                                             QELFSE-----PLPVAEVDQIARSIHRWIITKSRMWTD-GPAVYEATFTTIQ---ATRGK
                                                                                         ETIIADEFATGPLGLNELKHLSRSISRWV-----WRNFTPETFRARQKAISLRGASKGG 275
                                                                                                                                                                                        AQALAYAAAVTEGLRRSVDGDKGYSGLITKNPEHTAWDSHW-VTDKLYTLDELRFWLEET 117
                                                                                                                                                                                                                                                       PSRISWSSTSTSRTHSCVRCGTETAGGLTPWLKTPF---KRARTRRVGARGAIYPHRVRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WVWRNFTPETFR----ARQKAISLRGASKGGKEGGHKGGIASGA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKNPLSTAHATLWGPADALYELRALAHTLDEI-HALPEAGNPRRNVTRS-TVGRNVTLFD 188
RSAEHRWG
                                                                                                                                              HAL-PEAGNPRRNVTRSTVGRNVTLFDTTRMWAYRAVRHSWGGPVAEWEHTVFEHIHLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YTHRNFTPETFAQYVADTHTPEIQATRGRKGGSK-SKRGTVATSA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTRMWAYRAVRHSWGGPVAEWEHTVFEHIHLLNETIIADEFATGPLGLNELKHLSRSISR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CKNP---CH----PEWQEVEWREEPYTLDELADYLDLSASARRSVDKNYGLGRNCYLFE
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                                                                                                                                                                                                                       -----LLARVEQGLCDVLGGDASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGRKWAYRAIRQGWPA-FSQWLDAVIQRVEMYNASLPV-----PLSPPECRAIGKSIAK
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235
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29.5%;
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Pred. No. 3.5e-16;
                                                                                                                                                                                                                                                                                    -GHIVYALKNPVCLTDAARRRPIN-------
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hypothetical protein 2 - Corynebacterium glutamicum C;Species: Corynebacterium glutamicum C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 C;Accession: S32700; S32199

20-Feb-1995 #text_change

03-Aug-1995

RESULT S32700

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C;Superfamily: Mycobacterium tuberculosis mbtE protein; acetate--CoA ligase C;Keywords: carrier protein; phosphopantetheine; phosphoprotein F;517-949-Domain: acetate--CoA ligase homology <ACL> F;964-1031/Domain: acyl carrier protein homology <ACP> F;996/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-1461 <COL>
A;Cross-references: GB:Z95208; GB:AL123456; NID:g3261747; PIDN:CAB08474.1; PIA;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skeltor Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, A;Title: Deciphering the biology of Mycobacterium tuberculosi A;Reference number: A70500; MUID:98295987
A;Accession: B70588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable polyketide synthetase mbtF [similarity] - C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 C;Accession: B70588
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A; Residues: 1-99 <SHI>
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A; Accession: $32700
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Best Local S
Matches 24
395
                                                                                                                                                                                                                                      122
                                                                                                                                                                                                                                                                                     219
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                                                                                                                                                                                                                                                                                                            74 SYYSMNRYTT-----TGHIYYALKNPVC--LTDAARRRPINLLARVEQGLCDVLG----
                                                                                                                                                                                                                                                                                                                                                                                                                          17 PLASAEKSGAYR---HVTRQRALELPYIEANPLVMQSLVITDRDASDADWAADLAGLPSP
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                                                                                                                                                                                                                                                                                TLLSPALADTPVQPGIPGRTEVRLDREATAELADAARTRGVTISTLVQMAWATTLSAFTG
                                        WGGPVAEWEHTVFEHIHLLNETI--IADEFATGPLGLNELKHLSRSISRW
                                                                                SYLGENEERAIAGIGEMEDTLLVYENEPPGEVVGTAEFVANGVTE----RPVALESLSHF
                                                                                                                                                                                                                                                                                                                                                                             PLFVSELLALYRAGGHVAALPAAPRPYRD----YIGWLAGRDQTASRAMWADHLNGLDGP 218
                                                                                                                                                                                    RGDVTFGVTVSGRPSELSGVETMIGLFINTVPLRVRLDARATVGGQCAVLQRQFAMLRDH
                                                                                                                                                                                                                                   -GDASYGHRITKNP-
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Similarity 41.4%;
24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 25.2
73; Conservative
PVTVAAHRSTGELTLLVEVLDGALGTMAPESLGRRVLAVLQRLVSRW
                                                                                                                                       ELRALAHTLDEIHALPEAGN-PRRNV--TRSTVGRNVTLFDTTRMWAYRAVRHS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.1%; Score 98; DB 2; Length 1461 25.2%; Pred. No. 8.2;
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Pred. No. 0.17;
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SGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASDADWAADLAGLPSPSYVSMNRVTT 83

AGAVSTVSFSRAVQLTILAARPRVV--YVLESR------PGGEGVAMAR---

90

TGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYGHRITKNPLSTAHATLW 143

Query Match Best Local S Matches 55

55; Conser

5.9%; Score 93.5; Dilarity 25.3%; Pred. No. 1.8; Conservative 29; Mismatches

ВВ

Length

08 2;

Gaps

9;

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84 50 24

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e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushime y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R. A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6. A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Accession: E97944
A;Cross-references: DDBJ:AP000060; NID:g5104188;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1047
                                                                                                                                                              R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamaza DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeor A;Reference number: A72450; MUID:99310339
A;Accession: H72703
                                                                                                                                                                                                                                                                                                                probable translation initiation factor eIF-2B APE1047 - Aeropyrum pernix (strain C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999 C;Accession: H72703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE007317; PIDN:AAK99385.1; PID:g15458161; GSPDB:GN00174 C;Genetics:
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A; Residues: 1-1876 < KUR>
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                                                                                               A; Molecule type: DNA
A; Residues: 1-228 <KAW>
                                                                                                                                             A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 6.1%; Score 97.5; D
Local Similarity 19.3%; Pred. No. 13;
Local Similarity 43; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MWGYYGYEN---GFIPYVSNKLKGAANKENKGLLGDDFIIKKVSKNQFQNLEEWKKHW 1793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MWAYRAVRHSWGGPVAEWEHTVFEHIHLLNETIIADEFATGPLGLNELKHLSRSISRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEK-LDSREKIDSYMKNYNESMMMLDYLEASAVIRQNLSDNSKWFKKMDKEWRTN---- 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENNFYTLHGM---PKNGRYRTEGFDSSYQPVNMM--AGVFGGNTSKSTYGSISFKHNAFR 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAGNPRRNVTRSTVGRNVTLFDTTR 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108;
                                                                      PIDN:BAA80032.1; PID:d1043818;
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J.; Matsushima,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---DKLV 1683
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, P.; McAhren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249
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spindle assembly checkpoint protein SLDA - Emericella nidulans (Species: Emericella nidulans, Aspergillus nidulans C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change C;Accession: T09224 R;Efimov, V.P.; Morris, N.R. submitted to the EMBL Data Library, November 1997 A;Reference number: Z16619 A;Accession: T09224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: T37217
R;Oliver, K.; Harris, D.; Parkhill, submitted to the EMBL Data Library,
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A;Accession: T37217
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-606 <OLL>
A;Residues: 1-605 <OLL>
A;Cross-references: EMBL.AL031514; PIDN:CAA20595.1;
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable ATP/GTP binding protein - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 #sequence_revision
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A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-1216 <EFI>
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Best Local S
Matches 67
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les 67; Conserv
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                                                                                                                                                                                                                                                                                                                                    -----FTTPQYGAGALAVG-RG-SRGGTTGHHLPGALEELRVWTGAMSADQVRSQVLGG
                                                                                                                                                                                                                                                                                                   L 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTRQRALELPYIEANPLVMQSLVITDRDASDADWAADLAGLPSPSYVSMNRVTTTGHIVY 89
                                                                                                                                                                                                                                                                                                                                                                       RWVWRNFTPETFRARQKAISLRGASKGGKEGGHKGG-----IASGASRRAHTRQQFLEG
                                                                                                                                                                                                                                                                                                                                                                                                                             RMWAYRAVRHSWGGDV--AEWEHTVFEHIHL-LNETIIADEFATGPLGLNELKHLSRSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAT--LWG--PADALYE---LRALAHTLDEIHALPEAGNPRRNVTRSTVGRNVT-LFDTT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESSWALWAVKPADGVYQWKFTRTAVGADGKVTQSAEA--PGGDIAETDTWVQVTGVFDAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EENNALVLDGSAGYASATGPVVDETGSFTVSARVQLDSAKLASKPVGYEALVAGQQASAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALKNPVCLTDAA-----RRRPINLLARVEQGLCDVLGGDASYGHRITKNPLSTA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITQQAQLLEEGVPANELVAQ----WDAASSTGTTVKELSSYPAPSLT----LSAAGAVLD 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----DVEYPVFEPIPLRLVSYIATELGGGRAGVEPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEAVAVFESYKI-------VSRACVWEGV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 89.5; DE
Pred. No. 14;
38; Mismatches
                                  from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.; Barrell, B.G.; Rajandream, M.A. September 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-Dec-1999 #text_change 03-Dec-1999
                                  GB/EMBL/DDBJ
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                                                                                                                                      #text_change
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                                                                                                                                        11-Jun-1999
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A;Gene: sldA
A;Introns: 331/3; 477/1
C;Keywords: microtubule;
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A;Experimental source: strain R153
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Heldelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.J.; Bass, S.; Qin, I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTX toxin RtxA VC1451 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: C82199
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                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-4558 <HEI>
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                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB: AE004223;
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Best Local S
Matches 66
                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                       Matches
                                    2446
                                                                                                   2386 ASKGQPPVKNPKSSASANHKAEWLMTQHAEQWAKITAPYTDNHETLTSTKLASNDKEELH 2445
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     216
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                                                                                                                                   ASYGHRITKNP------LSTAHATLWGPADALY-----ELRALAHTLDEIH 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLASAEKSGAYRHVTRQRALELPYIEANPLVMQSLVITD------RDASDADWAAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DASYGHRITKNPLST-AHATLWGPADALYELRALAHTLDEIHALPEAGNPRRNVTRSTVG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTANRSGSSSLR------VPSPTKDSNP---QGTIIKDTLCNPIDRSIRDTILQELHTT 785
 HIHLLNETIIADEFATGPLGLNELKHLSRSISRWVWRNF---
                                  ALGETSNLENNKQQENVASIINTMLNDMLPFYALRTERNLLVQEGDEGFEVRAWPGTEDK 2505
                                                                  ALPEAGNPRRNVTRSTVGR--NVTLFDTTRMWAYRAVRH-----SWGGPVAEWEHTVFE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELFRTIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERSY---IIRRELGAGAYAPVY------LAESIDNLDSDSEMESVGSNSGRSTVS 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAAYPGYHAHPD-----TQSH--YAPEIERFMKSSSKRSRSGGEAAFDVPIIDPPGG 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAGLPS----PSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETFRARQ 263
                                                                                                                                                                       50;
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                                                                                                                                                                       Conservative
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23.6%;
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21.5%;
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                                                                                                                                                                  Score 89; DB; Pred. No. 2e+0; Mismatches
                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                         GB:AE003852; NID:g9655942; O1; strain N16961; biotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 89;
Pred. No.
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                                                                                                                                                                                     DB 2;
2e+02;
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37;
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TPETFRARQKAISLR 269
                                                                                                                                                                      Indels
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El Tor
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H.; Dragoi,
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I.; Sellers
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C; Superfamily: alanine transaminase

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RESULT 13
T14611
T14611
alanine transaminase homolog - Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genet:
A;Gene:
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A;Reference number: 221608
A;Accession: T36509
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                        R;Andersson, B.; Aslund, L.; Pettersson, U. submitted to the EMBL Data Library, March 1998 A;Description: 93.4 kb of complete sequence fro A;Reference number: 218159
A;Accession: T14611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T36509
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C:Species: Streptomyces coelicolor
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A; Residues: 1-303 <SAU>
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                                  A; Molecule type: DNA
A; Residues: 1-409 <AND>
                                                                  A; Status: preliminary; translated
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                   ;Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VITDRDA----SDADWAADLAGLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPRPTARPVTWAREDPPGGGPLAALAAGLRHTTAEYVLVASADLPFL-AGPTVGRLLSAL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSFETLFPESWLPRKPLAS---AEKSGAYRHVTRQRAL----ELPYIEANPLV---MQSL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                          FATGPLGLN-----ELKHLSRSISRWVWRNFTP-ETFRARQKAISLRGASKGGKEGGHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GASKGGKEGGHKGGIASGASRRAHTRQQFLEG
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75; Conservative
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                   EMBL: AF052832; NID: g3063540; PID: g3063548; PIDN: AAC14084.1
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23.5%;
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                                                                        from GB/EMBL/DDBJ
                                                                                                                            sequence from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , s.D.; Parkhill, J.;
July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DTW-DDLATARARIREHGHVLDEWISA--
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                                                                                                                            Trypanosoma cruzi
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291
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YNTDTVLASLHSTSKGIIG-ECGRRGGYFCLTNFPAPVREQVLK
                           FRARQKAISLRGASKG--GKEGGHKGGIASGASRRAHTRQQFLE
                                                                                                                                                                        A-SSGVRLLLQ-----VLVGDASDAVMVPIPQYPLYTAQLTLLGGTPAMYYLCEKDNW
                                                                                 RHSWGGPVAEWEHTVFEHIHLLNETIIADEFATGPLGLNELKHLSRSISRWVWRNFTPET
                                                                                                                ALNVEELASVYDECVAKNNATPRVLVVINPGNPTGGVLDRDVMEAVAKFCCDR
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                                                                                                                                                                                                                                                             ASDADWAA----
                                                                                                                                                                                                                                                                                         RAALATPEGKAKYPFSSIVYCNIGNPQALEQKPLTFFRQVMSLIDA-PFLLENEKVTSQY 91
                                                                                                                                                                                                                                                                                                                      RKPLASAE-----KSGAYRHVTRQRALE------LPYIEANPLVMQSLVITDRD 57
                                                                                                                                                                                                   ARRRPINLLARVEQGLCDVLGGDASYGHR--ITKNPLSTAHATLWGPADALYEL-----
                                                                                                                                           ----RALAHTLDEI----HALPEA-----GNPRRNVTRSTVGRNVTLFDTTRMWAYRAV 198
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                                                        --GIVLMADEVYQENVYAAGKRFLS--FREVVLGL
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23.3%;
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Pred. No. 12;
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                                                                                                                256
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C;Superfamily: nitrogen assimilation regulatory protein ntrC; response regulator homo C;Keywords: DNA binding; nucleotide binding; P-loop; phosphoprotein; transcription re F;5-114/Domain: response regulator homology <RRH>
F;143-336/Domain: RNA polymerase sigma factor interaction domain homology <SFI>
F;171-178/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulatory protein ntrC - Rhodobacter on Alternate names: regulatory protein n C; Species: Rhodobacter capsulatus C;Date: 07-Jun-1990 #sequence_revision C;Accession: S03321; S37299; S34983
                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X72382; NID:g313162; PIDN:CAA51075.1; PID:g313166 R;Foster-Hartnett, D.; Cullen, P.J.; Gabbert, K.K.; Kranz, R.G. Mol. Microbiol. 8, 903-914, 1993 A;Title: Sequence, genetic, and lacZ fusion analyses of a nifR3-ntrB-ntrC A;Reference number: S34980; MUID:93360820
                                                                                                                                              A; Gene: ntrC; nifRl
C; Superfamily: nitro
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A; Residues: 1-457 < KRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Gen. Genet. 215, 507-516, 1989
A; Title: The DNA sequence of the Rhodobacter
A; Reference number: S03318; MUID:89218961
                                                                                                                                                                                                      C; Genetics:
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A; Residues: 334-449 <FOS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Kranz,
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A; Residues: 1-457 < JON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL Data ce number: S37299
site: phosphate
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hypothetical protein C - Corynebacterium glutamicum plasmid pGA1
C;Species: Corynebacterium glutamicum
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 22-Oct-1999
C;Accession: $60675
R;Nesvera, J.; Patek, M.; Hochmannova, J.; Abrhamova, Z.
submitted to the EMBL Data Library, August 1995
A;Description: Complete nucleotide sequence of the cryptic plasmid pGA1 from Corynebacte A;Reference number: $60673
A;Accession: $60673
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A;Molecule type: DNA
A;Residues: 1-487 <NES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 59
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                                                                                                                                                                                                                                                        197 RWPLHVSDDPTAYKWHCQHDRVDRLADLMEIART-----MTGSQKPKKYIEQDFSSGRA
                                                                                                                                                                                                                                                                                                                                          138 APAWIGVNPLSGKCQLIW-LIDPVYAAAGKTSPNMRLLAATTEEMTRVFGADQAFSHRLS 196
                                                                                  311 QLKAAGERLKDAKIIDAYEVAYNVAQAVGADGREPDLPAMRDRLTMARRVRGYVAKG-QP
                                                                                                                                                                                                                    176
                                                                                                                                                                                                                                                                                                    132 KNPLSTAH---ATLW----GPADALYELRALAHTLDEIHALPEAGNPRRNV----- 175
370 VVPARRVETQSSRG-RKALATMGRRGAATSNARRWADPESKYAQETRQRLAE 420
                                                                                                                                                                     251 RIEAAQRATAEAKALAILDASLPSALDASGDLIDGVRVLWINPERARDETAFRHALTVGY 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 ETSRPEG--TDLPLVGRTAAMQALYRLVARVMNADLPVMIMGESGTGKSLIAKAI----H 185
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                                                                                                                                                                                                                                                                                                                                                                                   72 SPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYGHRIT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 59; Conserv
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                                          ETFRARQKAISLRGASKGGKEGGHKGGIASGASRRA-----HTRQQFLE 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NPV------CLTDAARRRPINLLARVEQGLCDVLGGDASYGHRITKNPLSTAHAT 141
                                                                                                                                                                                                             ----TRSTV-GRNVTLEDTTRMWAYRA-----VRHSWGGPVAEWEHTVFEHI-----
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                                                                                                                             -----HLLNETIIADEF------ATGPLG-----LNELKHLSRSISRWVWRNFTP 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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8; Mismatches
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Search completed: October 4, 2002, 15:35:15 Job time: 127 sec

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Run õ protein - protein search, using

October 4, 2002, 15:33:08; Search time 15.85 Seconds (without alignments) 740.191 Million cell updates/sec

Sequence: Title: Perfect score: US-09-720-583A-2 1596 1 MDSFETLFPESWLPRKPLAS.....IASGASRRAHTRQQFLEGLS 303

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 105224

105224 seqs, 38719550 residues

Minimum DB Maximum DB seq seq length:

0 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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P16218 clostridium P98161 homo sapien P04026 hamster int Q06990 papio hamad P24555 escherichia P162894 mouse intra Q06220 mycobacteri Q99y23 mus musculu P96963 pseudomonas Q9h254 homo sapien Q27355 methanobact P10377 escherichia Q06564 mycobacteri Q44471 agrobacteri Q44471 agrobacteri Q4471 grobacteri P47041 saccharomyc P31147 bacillus sp Q9cd72 mycobacteri P52377 bovine herp Q05318 ebola virus Q12432 saccharomyc Q49127 methylobact Q349127 methylobact Q349137 saccharomyc Q49127 sarcharomyc Q49127 methylobact Q340496 agrobacteri Q91dh0 arabidopsis Q10576 caenorhabdi P17632 rhodocyclus P23337 saccharomyc P89509 t genome po P41754 phytophthor		

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ALIGNMENTS

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InterPro: IPR001092; HLH_dim.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
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11. A1060765; -; NOT_ANNOTATED_CDS.

11. A1132428; -; NOT_ANNOTATED_CDS.

12. AA475250; -; NOT_ANNOTATED_CDS.

13. AA498625; -; NOT_ANNOTATED_CDS.

14. A1386259; -; NOT_ANNOTATED_CDS.

15. A1386259; -; NOT_ANNOTATED_CDS.

16. A1386281; -; NOT_ANNOTATED_CDS.

17. A1386281; -; NOT_ANNOTATED_CDS.

18. A1595781; -; NOT_ANNOTATED_CDS.

19. A1786503; -; NOT_ANNOTATED_CDS.

10. A1786503; -; NOT_ANNOTATED_CDS.

10. A1786503; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sterol levels.
MISCELLANEOUS: SREBPs have to be in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            site-1 protease.
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH)
TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: Under sterol-depleted conditions, SREBPs are cleaved sequentially by site-1 and site-2 protease. The first cleavage occurs within the luminal loop and is directly regulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sterols. The second cleavage by site-2 protease occurs within the first transmembrane stretch and liberates the soluble transcription factor. Cleavage by the cysteine proteases, caspase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: ISOFORM SREBP-1C PREDOMINATES IN LIVER, ADRENAL GLAND, BRAIN AND ADIPOSE TISSUE, WHEREAS ISOFORM SREBP-1A PREDOMINATES IN SPLEEN. BOTH ISOFORMS ARE FOUND IN KIDNEY, THYMUS TESTIS, MUSCLE, JEJUNUM, AND ILEUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and caspase-7, is induced during apoptosis, independent
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1 477 CYTOPLASMIC (POTENTIAL).
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this statement is not removed.
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TRANSCRIPTIONAL ACTIVATION
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P09432;
                                                                                                                                                            "Sequence, genetic, and lacz fusion analyses o operon in Rhodobacter capsulatus";
Mol. Microbiol. 8:903-914(1993).
                                                                                                                                                                                                                   MEDLINE-93360820;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-SB1003;
                                                                                                                                                                                                                                                                                                                                                                                                        Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
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01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
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                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                     DNA sequence of the Rhodobacter analogues required for nitrogen
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                                                     TKT_RHOCA STATE
Q52723; O68024;
Q52723; O68024;
30-MAY-2000 (Rel. 39
30-MAY-2000 (Rel. 39
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pfam; pF00158; Sigma54_activat; 1.
SMART; SM00382; AAA; 1.
SMART; SM00448; REC; 1.
                      Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
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             Rhodobacter
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75; Conserv
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PS00675; SIGMA54_INTERACT_1; 1.
PS00676; SIGMA54_INTERACT_2; FA
PS00688; SIGMA54_INTERACT_3; 1.
PS50045; SIGMA54_INTERACT_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fixation; Transcription regulation; Repressor; Activator; ing; ATP-binding; Phosphorylation; Sensory transduction.

1 118 RESPONSE REGULATORY.
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IPR001789; Response_reg.
IPR002078; Sig54_interact.
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                                                                                                                      STANDARD;
                                                          . 39, Created)
. 39, Last sequence up.
. 40, Last annotation (C 2.2.1.1) (TK).
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343 S
178 A
444 H
50042 MW;
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Pred. No. 3.3;
28; Mismatches
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H-T-H MOTIF (BY SIMILARITY); 7EB04B4FE4740306 CRC64;
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SIGMA-54 FACTOR INTERACTION (POTENTIAL)
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Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).

-i CAPALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyce 3-phosphate - D-ribose 5-phosphate + D-rylulose 5-phosphate - COFACTOR: THIAMINE PYROPHOSPHATE.

-i PATHWAY: KEY ENZYME OF THE REDUCTIVE AND THE OXIDATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF(
PROSITE;
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HSSP;
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SEQUENCE FROM N.A.
STRAIN-ATCC 33303 / B10;
MEDLINE-96186907; PubMed-8635754;
Sury D'Aspremont R., Toussaint B., Vignais P.M.;
"Isolation of Rhodobacter capsulatus transketolase: sequencing of its structural tktA gene.";
Gene 169:81-84(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00801; TRANSKETOLASE_1; 1.
PROSITE; PS00802; TRANSKETOLASE_2; 1.
Transferase; Thiamine pyrophosphate.
CONFLICT 376 382 PETIGGS -> LRNHRRL (IN REF. CONFLICT 484 484 A -> T (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restricted by the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Pfam; PF00456; transketolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHATE PATHWAYS.
-!- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.
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Vlcek C., Paces V., Maltsev N., P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                            305 KGAAERAEWEARLAALPAG--KRAEFERQMARGVA
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                                                                                       RGASKGGKEGGHKGGIASGASRRAHTRQQFLEGLS
                                                                                                                     VDCKTLIGFGSPNKADSYAVHGAPLGDAEIK-LTREAYGWEHGPFVIPAEIKAEWEAIGA
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                                                                                                                                                                               ITIDGRVTVSDVTDQKARFA-----ASGWDVLSCDGHDAEDIDRALTAAKKAKRPVL
                                                                                                                                                                                                               STVGRNVTLFDTTRMWAYRAVRHSWGGPVAEWE-----HTVFEHIHLLN------
                                                                                                                                                                                                                                           WVIAGDGCIMEGISQEAIGLAG------KQELDNLIVLWDNNN------
                                                                                                                                                                                                                                                                        -VLGGDASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAGNPRRNVTR 177
                                                                                                                                                                                                                                                                                                        WGARMAG--HPEYGHLEGVETTTGPLGQGISTAVGMAIAEK----SMAARFGKKLVDHKI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00456; transketolase; 1. PF02780; transketolase_C; 1. PF02779; transket_pyr; 1.
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                                                                                                                                                                                                                                                                                                                                                                      61;
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               484
672 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 72436 MW;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                    Pred.
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5-phosphate.
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Best Local Similarity
Matches 48; Conser
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ACT_SITE
DOMAIN
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SEQUENCE
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PROSITE; PS004018; EE_HAND; UNKNOWN_1.
PROSITE; PS00448; CLOS_CELLULOSOME_RPT;
PROSITE; PS00659; GLYCOSYI_HYDROL_E5; 1.
                                                                                                                                                                                                                                                                                                                  InterPro;
InterPro;
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Clostridium
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Clostridium thermocellum.
Clostridium thermocellum.
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PIR; JH0157; JH0157.
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MEDLINE-90323606;
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15-JUL-1998 (Rel.
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P16218;
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"Nucleotide sequence and deletion analysis of the cellulase-encoding
gene celf of Clostridium thermocellum.";
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110kages in cellulose.

DOMAIN: A 24 RESIDUES DOMAIN IS REPEATED TWICE IN THIS ENZ
WELL AS IN OTHER C.THERMOCELLUM CELLULOSOME ENZYMES, THIS
WAY FUNCTION AS THE BINDING LIGAND FOR THE SL COMPONENT.

SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULAS
A (FAMILY 5 OF GLYCOSYL HYDROLASES),
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e celh of clostridium thermocettum. , s 89:61-67(1990).

FUNCTION: THIS ENZYME CATALYZES THE ENDOHYDROLYSIS OF FUNCTION: THIS ENZYME CATALYZES, LICHENIN AND CEREAL
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EYNTVDIKNGKADAYITRMAQDMKAYGKEIWLRPLHEANGD-WYPWAIGYSSRVNTNETY
                         EQGLCDVLGGDA-----
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655 900
460 460
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833 856
833 856
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IPR001547; Glyco_hydro_F5.
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annotation update)
(EC 3.2.1.4) (EGH)
                                                                                                          MW.
                                                 26;
                                              Score 85; DB
Pred. No. 12;
6; Mismatches
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                       -SYGHRITKNPLSTAHATLWGPADALYELR----
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NUCLEOPHILE (BY SIMILARITY).
2 X 24 AA APPROXIMATE REPEATS
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PRO/THR-RICH (LINKER).
CELLULOSE-BINDING (BY SIMI
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PKD1_HUMAN
P98161;
                                                                                                                                                                                                                                                          Ward C.J., Peral B., Hughes J., Thomas S., Gamble V.,
Maccarthy A.B., Sloane-Stanley J., Buckle V.J., Kearney L.,
Higgs D.R., Ratcliffee P.J., Harris P.C., Roelfsema J.H.,
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"The polycystic kidney disease 1 gene encodes a 14 kb transcr
lies within a duplicated region on chromosome 16. The European
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VARIANTS
F-4190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34,
01-OCT-1996 (Rel. 34,
01-MAR-2002 (Rel. 41,
                                                  gene
                                                                                    VARIANT ADPKD 3748-ARG--VAI
MEDLINE=96108969; pubMed=88
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                                                                                                                                                      "The structure of a PKD domain from polycystic kidney_disease.";
                                                                                                                                                                                MEDLINE-99107746; PubMed-9889186; Bycroft M., Bateman A., Clarke J., Thomas R.L., Chothia C.;
                                                                                                                                                                                                                                                  Cell
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 2769-4303 FROM MEDLINE=94273192; PubMed=80
                                                                                                                                                                                                                                                                                                                                                                                                                                            "Polycystic kidney disease: the complete structure of the PKD1 gene and its protein."; Cell 81:289-298(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=95254638; PubMed=7736581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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            ADPKD
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; Metazoa; Chordata; C
---+heria; Primates; C
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                                                         Harris P.C.;
the 3' region of the
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precursor (Autosomal domina
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                                                six novel
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969; PubMed=8554072;
          P-2993; R-3016 AND V-3511,
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PubMed=8004675;
                                   ovel mutations."
58:86-96(1996).
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European
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                                                                                                                                                                                      A.
                                                                                                                                                                                                                                  Thomas R.L.,
Sandford R.;
                                                                                                                                                                                                                                                       VARIANTS ADPKD L-324 AND MEDLINE=99294580; PubMed
                                                                                                                                                                                                                                                                                                                                                                                          "Novel and disease) go
                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT ADPKD ASP-4032, MEDLINE-98180892; PubMe
                                                                                                                                                                   VARIANTS
                                                                                                                                                                                                          dominant polycystic
                                                                                                                                                                                                                        "Identification
                                                                                                                                                                                                                                                                                                                                               MEDLINE=99118881; PubMed=9921908;
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                                                                                                                                                                                        J. Hum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unusual pattern of mutation in the duplicated ealed by use of a novel strategy for mutation of Mol. Genet. 6:1473-1481(1997).
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=97403939; PubMed=9259200;
.E., Rossetti S., Bresin E
                                                                                                                                                                                                                                                                                                                                                           ADPKD MET-3375
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, Lens X.
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                                                                                                                                                                                                          of mutations in the
stic kidney disease
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lontek K.B., Corda
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                                                                                                                                                                                                                                                       324 AND S-845, AND PubMed=10364515;
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Pubmed=9521593;
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kidney diseas
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                                                              G-4136
                                                                                                                                                                                                         repeated part of type 1 gene, PKD1,
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Germino G.G.;
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                               mutations
                                                              AND C-4154,
                                                                                                                                                                                                                                                                                                                                    G., Hadjigavriel
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VARIANTS ADPKD SER-1100; ON THE PROPERTY AND ASN-2604 AND VARIANTS HIS-1995 AND ASN-2604 MEDLINE-20467506; PubMed=11012875; P
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                                                                                                                                                                                                                                                                                               VARIANTS ADEKD TRP-3753 AND ASN-3815.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS ADPKD GLN-3719 AND PRO-3852, MEDLINE=20514565; PubMed=11058904; Aguiari G., Savelli S., Garbo M., Boz
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MEDLINE=20311156; PubMed=10854095;
Mercier B., Quere I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  population.
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genes.";
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AND LEU-3193.
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nn R., Demetri
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G-2888; I-2905;
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Query Match Best Local Similarity

5.3%; 21.1%;

Score Pred.

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RESULT
POL_IPHA
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Best Local S
Matches 69
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P04026;
23-OCT-1986 ()
23-OCT-1986 ()
16-OCT-2001 ()
Putative POL )
                                                                                                                                                                                                                  Endonuclease; ESFOUENCE 863
                                                                                                                                                                                                                                                                             Pfam; PF02022; Integrase_Zn; Pfam; PF00075; rnaseH; 1. Pfam; PF00665; rve; 1. Pfam; PF00078; rvt; 1.
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003308; Inte
InterPro; IPR002156; RNas;
InterPro; IPR000477; RVTs;
InterPro; IPR001584; Rve
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                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00552; integrase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene: close evolutionary relationship types B and D oncovirus genes.";
J. Virol. 55:387-394(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ono M., Toh H., Miyata T., Awaya T.;
"Nucleotide sequence of the Syrian hamster intracisternal A-particle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=85264989; PubMed=2991563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses;
                                                                                                                                                                                                                                                             Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hamster intracisternal a-particle (IAP-H18).
Viruses; Retroid viruses; Retroviridae; Int
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcriptase
                            420
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                                                             KSGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASDADWAADLAGLPSPSYVSMNRVT 82
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                          KTGLGAYVVKDRVISKQYNETSPQVVECLIVLE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FETLFPESWLPRKPLASAEKSGAYRHV---
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                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001037; Integrase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 02, Created)
(Rel. 02, Last sequence update)
(Rel. 40, Last annotation update)
)L polyprotein [Contains: Endonuclease, se (EC 2.7.7.49)].
                                                                                                                                                                                                               RNA-directed DNA
; Polyprotein.
363 AA; 97036 MW;
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                                                                                                                              Score 83.5;
Pred. No. 1
                                                                                                                                                                                                                                                         polymerase; Hydrolase; Nuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                           Mismatches
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                                                                                                           110;
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                        -VLEAFPGP----LNIVS 465
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01-FEB-1995 (Rel. 3
01-FEB-1995 (Rel. 3
01-MAR-2002 (Rel. 4
Acrosomal protein 9
Signal;
SIGNAL
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                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                                          Freemerman A.J., Wright R.M., Flickir "Tissue specificity of the acrosomal vaccine candidate molecule.";
Biol. Reprod. 50:615-621(1994).
-I- SUBCELLUAR LOCATION: NASCENT ACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93183503; PubMed-8442953; Freemerman A.J., Wright R.M., Flickinger C.J., Herr J.C.; "Cloning and sequencing of baboon and cynomolgus monkey is acrosomal protein SP-10: homology with human SP-10 and a antigen (MSA-63).";
                                                                                                                        EMBL; S56458; AAB25693.1; -.
                                                                                                                                                                                                                                                                                                                                                            -i- ALTERNATIVE PRODUCTS: 2 ISO
SHORT FORM; ARE PRODUCED BY
-i- TISSUE SPECIFICITY: TESTIS.
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TISSUE=Testis;
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Papio hamadryas (Hamadryas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
MEDLINE=94220578;
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                                                                                                                                                                                   s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                  Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Metazoa; Chordata;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dev.
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71
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. 31, Last sequence upd
. 41, Last annotation u
n SP-10 precursor (Acro
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POTENTIAL.

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P24555; P78068;
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                                         STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna
Riley M., Collado-Vides J., Glasner J.D., Rode C.;
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.
                                                                                                                                                        Kanatani A., Masuda T., Shimoda T., Yoshimoto T., Tsuru D.;
"Protease II from Escherichia coli: enzyme gene and characterization of J. Blochem. 110:315-320(1991).
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nce 277:1453-1474(1997).
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Encogene; EG11004; ptrB.

InterPro; IPR001375; Peptidase_S9.

InterPro; IPR001375; Peptidase_S9_N.

InterPro; IPR004106; Peptidase_S9_N.

InterPro; IPR002470; Prol_endopep_ser.

InterPro; IPR002470; Proligo_PTase.

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Pfam; PF00326; Peptidase_S9_N; 1.
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InterPro; IPR000477; RVTse.
InterPro; IPR001584; Rve.
Pfam; PF00552; Integrase; 1.
Pfam; PF02022; Integrase_Zn; 1
Pfam; PF00075; rnaseH; 1.
Pfam; PF000655; rve; 1.
Pfam; PF00078; rvt; 1.
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InterPro;
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Mouse intracisternal a-particle (IAP-IL3).
Viruses; Retroid viruses; Retroviridae; Intracisternal A-particles.
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01-OCT-1989 (Rel.
01-NOV-1995 (Rel.
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Nucleic Acids Res. 14:5901-5918(1986).
  577
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SSFGKLQYLHVSIDTCSGIMFASPLTGEKASHVIQHCLEAWSAW
                                                                                                     TAETLRSRFSLTRKEARDIVTQCQSCCEFLPVPHVGINPRGIR-----PLQVWQMDVTHV
                                                                                                                                                        LPEAGNPRRNVTRSTVGRNVTLFDTTRMWA-----YRAVRHSWGGPVAEWEHTV---
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IPR003308;
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4 AA; 91000 MW; A369620A450F729A CRC64;
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32, Last annotation
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: RNaseH.
: RVTse.
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19.0%;
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-particle genome inserted
cell line WEHI-3B.";
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DT 15-JULI
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RN STRAIN
RX COLE &
RA GOIGOR
RA FLELS
RA FLELS
RA FLELS
RA FOLOR
ROCC -!- SI
CCC -!- SI
CC
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr:
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyo
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
InterPro; IPR000713; Mur_ligase. InterPro; IPR0004101; Mur_ligase_C. Pfam; PF01225; Mur_ligase; 1. Pfam; PF02875; Mur_ligase_C; 1. Peptidoglycan synthesis; Cell divi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
UDP-N-acetylmuramoylalanyl-D-gluttamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase (EC 6.3.2.15) (UDP-MurNAc-pentapeptide synthetase)
(D-alanyl-D-alanine-adding enzyme).
MURF OR RV2157C OR MT2216 OR MTCY270.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: INVOLVED IN CELL WALL FORMATION. CATALYSES THE FI
STEP IN THE SYNTHESIS OF UDP-N-ACCETYLMURAMOYL-PENTAPEPTIDE,
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STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Gwinn M.L., Haft D., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg

Belchet M., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                           HSSP; P11880;
TIGR; MT2216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STEP IN THE SIMILARITY).

PRECURSOR OF MUREIN (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanyl-D-alanin

CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanyl-D-alanin
                                                                                                                                                                                                                                                                            Z95388; CAB08670.1;
AE007068; AAK46500.
                                                                                                                                                                                                                                                                                                                                                                            an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                           license agreement (See http://www.isb-sib.
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01-MAR-2002
01-MAR-2002
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                                                                                                                                                                                                                                                                            Bonne S., van Hengel J., Nollet F., Kools P., van Roy "Plakophilin-3, a novel armadillo-like protein present desmosomes of epithelial cells.", J. Cell Sci. 112:2265-2276(1999).

1- FUNCTION: MAY PLAY A ROLE IN JUNCTIONAL PLAQUES.

1- SUBCELLULAR LOCATION: Nuclear and associated with

1- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.

1- SIMILARITY: CONTAINS 8 ARM REPEATS.
                                          EMBL; AF136719; AJ MGD; MGI:1891830;
                                                                                                                                                                                                   the
                                                                                                                                                                          use
                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=99310799; PubMed=10381383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plakophilin
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                        InterPro;
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                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation. European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LDVSRLVVVG-TGRSISAMHHGAVLEGAWGSGEATADHGADRTAVNVADGDAALALL
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                                                                                                     non-profit institutions as long and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
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24; Mismatches
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RESULT 12
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Best Local Similarity
SEQUENCE FACE....

STRAIN-ATCC 15692 / PAO1;

STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brihkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou Hickey M.J., Brihkman F.S.L., Tolentino E., Westbrock-Wadman S., Yuan Y. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Spencer D.H., Wang G.K.-S., Wu Z., Paulsen I.T., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00185;
PROSITE; PS5017
Cell adhesion;
                                                                                                                                                                                                                                               STRAIN-FRD1;
STRAIN-FRD1;
Howell M.L., Heur M., Klotz M.G.,
"Pseudomonas aeruginosa oxidative
"Pseudomonas aeruginosa oxidative
"Oxidative" (MAR-1997) to the EMBL/C
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16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
DNA repair protein radA homolog (DNA r
RADA OR SMS OR PA4609.
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                                                           SPCQ_HUMAN STANDARD; PRT; 2564 AA.

99H254; Q9HCD0; Q9H3GB; Q9H1K9; Q9H1K9;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Spectrin beta chain, brain 3 (Spectrin, non-erythroid beta chain (Beta-IV spectrin).
SPTBN4 OR SPTBN3 OR KIAN1642.
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                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA repair;
ZN_FING
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                                               Homo sapiens (Human)
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-!- SIMILARITY: BELONGS TO THE RADA FAMILY
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ATP (POTENTIAL).

E -> K (IN REF. 1).

E -> D (IN REF. 1).

GR -> AA (IN REF. 1).
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Pred. No. 10;
Pred. No. 10;
Mismatches
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Pfam; PF00307; CH; 2.
Pfam; PF00455; PH; 1.
Pfam; PF00435; Spectrin; 18.
PR.NTS; PR00483; SPECTRINPH.
SWART; SM00203; CH; 2.
SMART; SM00233; PH; 1.
SWART; SM00150; SPEC; 16.
PROSITE; PS00019; ACTININ_1; 1
PROSITE; PS00020; ACTININ_2; 1
PROSITE; PS00020; ACTININ_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001715; (InterPro; IPR001849; InterPro; IPR002017; InterPro; IPR001605; INTERPRO; IPR001605; INTERPRO; IPR001605; IPR001715; IPR00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berghs S., Aggujaro D., Dirkx R. Jr., Maksimova i
Hermel J.-M., Zhang J.-P., Philbrick W., Slepnev
Solimena M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tse W.T., Tang J., Jin O., Korsgren C., John K.M., Kung Gwynn B., Peters L.L., Lux S.E.;
"A new spectrin, beta-IV, has a major truncated isoform associates with promyelocytic leukemia protein nuclear b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-21316449; PubMed-11294830;
                                                                                                                                                               Cytoskeleton;
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ALTERNATIVE PRODUCTS: 4 isoforms;
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'1.5; DP
        Methanobacteriales;
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SPECTRIN 18.

PH.

MISSING (IN ISOFORM 3).

AVQAAEGLLRQGNIYGEQAQEAVTRLLEK -> MPHYPSCS
SAPSIGTPIPPQIQULEARHR (IN ISOFORM 3).

NQENQLRAQQMQKLHDQLELQH -> CLIIHPALLHPPWE
PPYLPRSSS (IN ISOFORM 2).

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ENTC_ECCLI STANDARD; PRT; 391 AA. p10377; p77099; 01-MAR-1989 (Rel. 10, Created) 01-OCT-1994 (Rel. 30, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) 1sochorismate synthase entC (EC 5.4.99.6). ENTC OR B0593 OR 20735 OR ECS0632. Escherichia coli 0157:H7.
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Hadradge T., Bashizadeh R., Blakely D., Cook R., Gilbert K.,
Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).

--- FUNCTION. REMOYES THE AMINO-TERMINAL METHIONINE FROM NASCENT
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InterPro; IPR002468; MAP_2.
InterPro; IPR001714; Methamino_PTas;
InterPro; IPR001994; Peptidase_M24.
Pfam; PF00557; Peptidase_M24; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
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-!- CATALYTIC ACTIVITY: L-METHIONYLPEPTIDE +
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WEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., I
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DNA Res. 8:11-22(2001).
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SEQUENCE FROM N.A.
Allen E.,
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Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Le
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EMBL; AE005252; BAB34055.1; -.
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"Structural analysis of the 6-kb cryp
Rhodococcus erythropolis N186/21 and
Rhodococcus shuttle vectors.";
Microbiology 143:3137-3147(1997).
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Plasmid pT3.2I.
Bacteria; Proteobacteria;
                                                              MEDLINE=98015402; PubMed=9353918;
De Mot R., Nagy I., De Schrijver
Schoofs G. Vanderleyden J.;
"Structural analysis of the 6.kb
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EMBL; AJ007958; CAA07792.1; -.
InterPro; IPR004322; Replicase.
Pfam; PF03090; Replicase; 1.
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998 (TrEMBLrel. 05, Last sequence up
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REPLICATION PROTEIN.
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Pred. No. 3.6e-22;
D; Mismatches 129
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                                                                                                                                                     "Cloning and DNA sequence of the plasmid pAL5000."; Plasmid 27:130-140(1992). EMBL; M23557; AAA98171.1; EMBL; M60875; AAA25372.1; InterPro; IPR004322; Replicase.
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SEQUENCE 310
                                                                                        Plasmid.
SEQUENCE
                                                                                                                                                                                                                                                                  SEQUENCE OF 160-336 FROM N.A. SEQUENCE OF 160-336 FROM M.A. MEDLINE-92311251; PubMed-1615063; Labidi A., Mardis E., Roe B.A., W "Cloning and DNA sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q52148 PRELIMINARY; PRT; 336 AA. Q52148; Q49181; O1-NOV-1996 (TremBLrel. 01, Created) O1-NOV-1996 (TremBLrel. 01, Last sequence up 01-DEC-2001 (TremBLrel. 19, Last annotation HYPOTHETICAL 37.1 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                               Gene 71:315-321(1988).
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MEDLINE=89138007; PubMed=3224826;
Rauzier J., Moniz Pereira J., Gio
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e Mycobacterium fo
329; DB 2;
No. 6.1e-21;
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01-DEC-2001
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Q51635;
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SEQUENCE
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EMBL; D30060; BAA062981; -.
InterPro; IPR004322; Replicase.
InterPro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=95050306; PubMed=7525540;
Hiraga S., Sugiyama T., Itoh T.;
"Comparative analysis of the replicon
                                                                                                                                                                                                                                                                                                                                                                                                Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid ColE5-099.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Shigella sonnei.
                                                                                                                                                                                                                                                         Pfam; PF03090; Replicase;
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DSFETLFPESWLPRKPLASAE-KSGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASD
                                     GLICKNPFHLE---
                                                       HRITKNPLSTAHATLWGPADALYELRALAHTLDEI-HALPEAGNPRRNVTRS-TVGRNVT
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                                                                                A--PAPNITYKNPVNGHAHLLYALNIAVRTAPDASVKALKYAAAIERALCEKLGADVNYS
                                                                                                     AGLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYG
                                                                                                                             EENLPHRPYHTDDLAFGLRISGKGRALLAGYIQQNQPHAQFWLVFDVDREGAAIDWSDRN
                                                                                                                                                  ESWLPRKPLASAEKSGAYRHVTRQRALELPYIEANPLVMQSLVI--TDRDASDADWAADL
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93; Conserv
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Conservative 4
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                                    -W----LVMEWREEAYTLDELADYLDLSASARRSIDKHYGMGRNCH
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Last annotation updat
                                                                                                                                                                        Score 322.5; DB 2;
Pred. No. 2e-20;
7; Mismatches 121;
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RESULT
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AC Q5
DT 01
DT 01
DT 01
DT 01
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OC S1
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REP PROTEIN.
Shigella sonnei.
Plasmid ColE6-CT14.
Bacteria; Proteobacteria; shigella.
                                                                                                              Q51636;
Q51636;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
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J. Bacterio
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Q51631;
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EMBL; D30057; BAA06295.
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InterPro; IPR004322; Replicase.
InterPro; IPR001440; TPR.
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                                                                                                                                                                                                                                                                                                                   SIAKYTHRNFTPETF-AQYVATTHTPEIQAAR--GRKGGIAKGAGYEDKRSTALEMLVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRITKNPLSTAHATLWGPADALYELRALAHTLDEI-HALPEAGNPRRNVTRS-TVGRNVT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A--PAPNITVKNPVNGHAHLLYALNIAVRTAPDASVKALKYAAAIERALCEKLGADVNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EENLPHRPYHTDDLAFGLRISGKGRALLARYIQQNQPHAQFWLVFDVDREGAAIDWSDRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 AA;
                                                                                                           (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 19,
                                                                                                                                                                                                         PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176:7233-7243(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=7525540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -W----LVMEWREEAYTLDELADYLDLSASARRSIDKHYGMGRNCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35081 MW;
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19,
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                     gamma
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Last annotation updat
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Pred. No. 2.5e-20;
3; Mismatches 124;
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                     subdivision;
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                     Enterobacteriaceae;
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Best Local Similarity
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Q51639;
Q1-NOV-1996
  Plasmid.
SEQUENCE
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SEQUENCE
                                        J. Bacteriol. 176:7233-7243(1994).
EMBL; D30064; BAA06302.1;
InterPro; IPR004322; Replicase.
InterPro; IPR001440; TPR.
Pfam; PF03090; Replicase; 1.
                                                                                                                                                                                                          MEDLINE-95050306; Pu
Hiraga S., Sugiyama
                                                                                                                                                                                                                                                                                                                               Bacteria; Pı
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
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EMBL; D30061; BAA06299.1; -.
                                                                                                                                                                  plasmids.
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=95050306; PubMed=7525540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=624;
[1]
                                                                                                                                                                                       Hiraga S., Sugiyama T., 1
"Comparative analysis of
                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004322; Replicase.
InterPro; IPR001440; TPR.
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Comparative analysis of the replicon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SISRWVWRNETPETFR----ARQKAISLRGASKGGKEGGHK---GGIASGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEDTTRAWAYRAVRHSWGGPV-AEWEHTVEEHIHLLNETIIADEFATGPLGLNELKHLSR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A--PAPNITYKNPVNGHAHLLYALNIAVRTAPDASVRALKYAAAIECALCEKLGADVNYS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYG
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                                                                                                                                                                                                                                                                                                                                                  Proteobacteria;
    308
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    AA;
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                                                                                                                                                                                pubMed=7525540;
ma T., Itoh T.;
ysis of the replicon
    34851 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -W----LVMEWREEAYTLDELADYLDLSASERRSIDKHYGMGRNCH
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                                                                                                                                                                                                                                                                                                                                                gamma
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Last annotation update)
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  2245A0EA06FBF085 CRC64;
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Query Match Best Local S Matches 90

Similarity

19.8%; 30.9%;

90;

Conservative

48;

Score 316.5; DB (Pred. No. 6.9e-20) 8; Mismatches 12

124;

Indels Length

29;

Gaps

10

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from

a host vector system

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Length 302;

Indels

52;

12;

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29 EBJ46
1D BJ46
1D BJ70
10 DJ70
10 DJ
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Best Local Similarity
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01-OCT-2000
01-OCT-2000
01-DEC-2001
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Hirasawa K., Ishii Y., Kobayashi M., Koizumi K.,
"Improvement of Deulfurization Activity in Rhodoc
KA2-5-1 by Genetic Engineering.";
Biosci. Biotechnol. Biochem. 65:239-246(2001).
EMBL; AB040101; BAA92818.1; -.
InterPro; IPR004322; Replicase.
Pfam; PF03090; Replicase; 1.
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IAASIHRWIVTKSRMWAD-GPAVYEATFVAIQSARGRKWTEKK--
                                                                                                                                              VTLFDTTRMWAYRAVRHSWGGPVAEWEHTVFEHIHLLNETIIADEFA--TGPLGLNELKH
                                                                                                                                                                                                                           RITKNPLSTAHATLWGPADALYELRALA---HTLDEIHALPE--AGNPRRNVTRSTVGRN
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                                                 LSRSISRWV----
                                                                                                    CMLFETARTWAYRELRCHWGDP-----
                                                                                                                                                                                               LMTKNPTHSAWDTHWIHA----ETRSLADLEHDLGK-HMPPPRWRQSKRRREDPVGLGRN
                                                                                                                                                                                                                                                                                                 NHPLPNATVENPRNGHAHAVWALTEPFTRTEYARRKPLAYAAAVNEGLRRAVDGDAAYSG
                                                                                                                                                                                                                                                                                                                                             -LPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYGH
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                                                 -WRNFTPETFRARQKAI-SLRGASKGGKEGGHKGGIASGASRRAHT
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Last annotation update)
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Pred. No. 1.9e-19;
1; Mismatches 115;
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Best Local !
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SEQUENCE
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SPECIES-P.jensenii; STRAIN-DFI; PIASMID-
Stierli M.P., Meile L., Teuber M.;
Nolecular analysis of plasmid pLME106,
Propionibacterium jensenii.";
Submitted (OCT-1999) to the EMBL/GenBan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium jensenii, and Propionibacterium acidipropionici. Plasmid pLME106, and Plasmid pRG01. Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Propionibacterineae; Propionibacterium.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kiatpapan P.,
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Yamashita M., Murooka Y.;
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                    RPRARRA
                                                                                                                                                                                                                   GRNCAIFETARTWAYRDARRIRORHEY--PTAEDSADLHAVIASTVEALNAG--YSEPLP
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                                                                                                                                                                                                                                                                                                                   DASYAGLITKNPEHPAWNTTW-CTDHLYRLAELDTHLDAAGLMP-APSWRRTRRRNPVGL
                                                                                                                                                                                                                                                                                                                                                                    DASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAGNPRRNVTRSTV--
                                                                                                                                                                                                                                                                                                                                                                                                                   WL-----PNAIVENPDNGHAHAVWALEAAIPRTEYAHRKPIAYAAAVTEGLRRSVDG
                                                                   SGASRRA 292
                                                                                                                      AREAAGIAASIHRWITHRFYGWIDSHTVNEATFSTIQ
                                                                                                                                                                  LNELKHLSRSISRWVWRNF-----TPETFRARQKAISLRGASKGGKEGGHKG-GIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Environ. Microbiol. 66:4688-4695(2000). AJ250233; CAB88396.1; -. AB007909; BAB17919.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                       294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33908 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-DF1; PLASMID-PLME106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 306;
Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDFC0794EFCF2D30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302
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Propionibacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a plasmid isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLASMID=PRG01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piao Y.Z.,
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Best Local
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                                                                                                                                                                                          Q51632;
01-NOV-1996
01-NOV-1996
01-DEC-2001
                                                                                           Escherichia coli.
Plasmid ColE2imm-K317.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid 36:36-41(1996).
EMBL; U39878; AAB03568.1;
InterPro; IPR004322; Replicase.
Pfam; PF03090; Replicase; 1.
Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q45279
Q45279;
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Ankri S., Bouvier I., Reyes O., Predali
"A Brevibacterium linens pRBL1 replicon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid autonomous circular plasmid pRBL1.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Micrococcineae; Brevibacteriaceae; Bre
NCBI_TaxID=1703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TIEMBLIFEL 01, C
01-NOV-1996 (TIEMBLIFEL 01, L
01-DEC-2001 (TIEMBLIFEL 19, L
PLASMID PRBL1 PUTATIVE THETA
  SEQUENCE FROM N.A
                                            NCBI_TaxID=562;
                                                                        Escherichia
                                                                                                                                                                      REP PROTEIN.
                                                                                                                                                                                                                                                                                           Q51632
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                                                                                                                                                                                                                                                                                                                                                                                                                                      KGGIASGASRRAHTRQQFLEGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKRKNPV--GLGRNCTLFETVRWDVYRVARTI----RKRNEHPTPEDRHDLEAAIVNLCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEGLRRSVDGDKGYSGLITKNPTHDQWEASW-LTDHLYNLDELTEHLTVSDFMPPDSWQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFETLFPESWLPRKPLASAE-KSGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASDA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GMNSTFSEALPASEIRATIRSFYKWITTRYTGWLDSRTTSQSKSAAYHRNT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPRRNVTRSTVGRNVTLFDTTRMWAYRAVRHSWGGPVAEWEHTVFEHIHLLNETII----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQGLCDVLGGDASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMRAMWNRKAW------QPNAVVENPANGHAHAVWALAEPVTRTEYARRKPLAYAAAV
                                                                                                                                                                                                                                                                                                                                                                                                             KGGVVSGQVR----RQKALERVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ADEFATGPLGLNELKHLSRSISRWVWRNFT----PETFRARQKAISLRGASKGGKEGGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STET-WGQMWLPLWPLASDDLLQGIYR-TSRHNALELRYIEANPQSLSNLLVVDIDHPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity 32.8%;
06; Conservative
                                                                                                                                                                                       6 (TrEMBLrel. (6 (TrEMBLrel. (1 (TrEMBLrel. )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 AA;
                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DWAADLAGLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35266 MW;
                                                                                                                                                                                          01,
01,
19,
                                                                                              gamma
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Last annotation update)
A REPLICASE (ORF310).
                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 304; DB
Pred. No. 8.8e-
34; Mismatches
                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                             303
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                                                                                              subdivision;
                                                                                                                                                                                                                                                                                           311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
.8e-19;
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                                                                                              Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 310;
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Best Local S
Matches 90
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J. Bacteriol. 176: ...

EMBL; D30058; BAA06296.1; -..

EMBL; D300792; HTH_LuxR.

InterPro; IPR0007322; Replicase.

InterPro; IPR001440; TPR.

""03090; Replicase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                     Q51630;
Q51630;
01-NOV-1996
01-NOV-1996
01-DEC-2001
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                                                                                             Plasmid.
SEQUENCE
                                                                                                                 J. Bacteriol. 176:7233-7243(1994).

EMBL; D30056; BAA062941.; ".

InterPro; IPR000792; HTH_LuxR.

InterPro; IPR004322; Replicase.

Pfam; PF03090; Replicase; 1.
                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-95050306; Pu
Hiraga S., Sugiyama
                                                                                                                                                                                                                                                                       Escherichia coli.
Plasmid ColE2-CA42.
Bacteria; Proteobacteria;
                                                                                                                                                                             plasmids.";
                                                                                                                                                                                                                                                               Escherichia
                                                                                                                                                                                        "Comparative analysis of the replicon
                                                                                                                                                                                                                                                 NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95050306; PubMed=7525540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hiraga S., Sugiyama T., Itoh
Comparative analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                             232
                                                                                                                                                                                                                                                                                                                                                                                                                                                   246
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FPESWLPRKPLASAEKSGAYRHVTRQRALELPYIEANPLVMQSLVI--TDRDASDADWAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLICKNPFHLE----W----LVMEWREEAYTLDELADYLDLSASARRSIDKHYGMGRNCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFDTTRMWAYRAVRHSWGGPVAEWEHTVFEHIHLLNETIIADEFATGPLGLNELKHLSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HRITKNPLSTAHATLWGPADALYELRALAHTLDEI-HALPEAGNPRRNVTRS-TVGRNVT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A--PAPNITVKNPVNGHAHLLYALNIAVRTAPDASVKALKYAAAVERSLCEKLCADVNYS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EENLPHRPYHTDDLAFGLRISGKGRALLARYIQQNQPHAQFWLVFDVDREGAAIDWSDRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESWLPRKPLASAEKSGAYRHVTRQRALELPYIEANPLVMQSLVI--TDRDASDADWAADL 67
                                                                                                                                                                                                                                                                                                                                                                                                                          TAKYTHRNFTPETF----AQYVADTHTPETQAKRGRKGGTAKG----EAYDDKRFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                ISRWVWRNFTPETFRARQKAISLRGASKGGKEGGHKGGIASGASRRAHTRQQFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFEMTRKWAYRAIRQGWPA-FSQWLDAVIQRVEMYNASLPV-----PLSPPECRAIGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYG 127
                                   ch 19.0%;
Similarity 30.4%;
90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 68
                                                                                             311
                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                             A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                    PubMed=7525540;
ma T., Itoh T.;
                                                                                             35298 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35370 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.0%;
                                                                                                                                                                                                                                                                                                                     01,
01,
19,
                                                                                                                                                                                                                                                                        gamma
                                     55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                           Created)
                                  Score 303; DB 2;
Pred. No. 1.1e-18;
5; Mismatches 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 303.5; DB 2
Pred. No. 9.8e-19;
3; Mismatches 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              replicon
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                             F2E75BECA0D8A137 CRC64;
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                                                                                                                                                                                                                                                                         subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                   311
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Best Local Similarity
Matches 101; Conserv
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SEQUENCE
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Q9RLE8;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE REPLICON PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid.";
Plasmid 45:88-100(2001).
EMBL; AJ249644; CAB56518.1; -
InterPro; IRR004322; Replicase.
Pfam; PF03090; Replicase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-036:H34;
MEDLINE-21223402; PubMed-11322823;
MAVISON M.B., Walsh T.R., Bennett P.M.;
"PUB6060: a broad host-range, DNA polymerase-I-independent ColE2-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid p11184.
Bacteria; Proteobacteria;
Plesiomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 VTLFDTTRMWAYRAVRHSWGGPVAEWEHTVFEHIHLLNETIIADEFATGPLGLNELKHLS 243
294
                                                                229
                                                                                                                                                                                                                                                            182
                                                                                                                                                                                                                                                                                                                                                               124 ASYGHRITKNPLSTAH--ATLWGPADALYELRALAHTLDEIHALPEAGNPRRNYTRSTVG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 CHLFEMTRKWAYRAIROGWPA-FSQWLDAVIQRVEMYNASLPV-----PLSPPECRAIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 TLFPESWLPRKPLASAEKSGAYRHVTRQRALELPYIEAN-PLVMQSLVI-TDRDASDADW 63
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                                                             IAKSISKWTMVTYRSLGFDEYVKLTHSPEVQAYRGRRSKGGGRPSIGEPWLALGISRRSY
                                                                                                                                                                                           RNCTLFDKTRKWAYRAIRQGW-PEYSQWLQACIERAKAYNLQFSA-----PLDENEVMG
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                                                                                                                          LSRSISRWV------WRNFTPETFRARQKAISLRGASKGGKEGGHKGGIASGASRRAH 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.7%; Score 298; DB 2; Length 29 milarity 33.4%; Pred. No. 2.8e-18; Conservative 33; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FBDBEF09EEFBBCF2 CRC64;
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Search completed: October Job time: 179 sec 4, 2002, 15:36:07

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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length: 2000000000
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-08-460-751-2
US-08-191-879-2
US-08-928-361B-30
US-08-928-361B-6
US-08-928-361B-6
US-08-928-361B-6
US-08-928-361B-6
US-08-92-045-5
US-08-947-429A-3
US-08-947-452-4
US-08-9413-814-42
US-09-105-537-6
US-09-105-537-6
US-09-105-537-6
US-09-105-537-6
US-09-105-537-3
US-09-105-537-6
US-09-105-537-3
US-09-105-537-6
US-09-105-537-6
US-08-292-045-10
US-08-292-045-10
US-08-947-965-74
US-08-947-965-74
US-08-996-7930-1
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13, Appli
14, Appli
15, Appli
16, Appli
17, Appli
17, Appli
                 Matches
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Result No.

2002 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 |

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
72.5	72.5	72.5	72.5	72.5	72.5	72.5	73.5	73.5	74	74	74	74.5	75	75	75	75	75
4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.6	4.6	4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.7
1611	964	850	828	606	606	177	417	417	580	417	285	554	1837	1042	867	378	250
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US-08-804-227C-5	US-08-860-339-18	US-08-481-435-10	US-08-481-435-2	US-09-079-630-32	US-08-577-492-32	US-08-737-825-9	PCT-US92-06965A-25	US-08-867-611-20	US-08-672-564-1	US-08-672-564-9	US-08-292-045-7	US-08-943-714-2	US-08-928-361B-5	US-08-928-361B-11	US-08-938-365-2	us-09-500-569-10	US-09-216-295-14
Sequence 5, Appli	Sequence 18, Appl	Sequence 10, Appl	Sequence 2, Appli	Sequence 32, Appl	32,	9, A	Sequence 25, Appl	Sequence 20, Appl	Sequence 1, Appli	Sequence 9, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 11, Appl	Sequence 2, Appli	Sequence 10, Appl	Sequence 14, Appl

ALIGNMENTS

Maximum

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APPLICANT: DACKUMGA...
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: OLIN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
STREET: ONE MOUNTAIN ROAD
; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-658-136-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-658-136-5
                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
NAME: LASSEN, ELIZABETH
REGISTRATION UNMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEFAN: 508-872-8400
TELEFAN: 508-872-5415
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
IFENCETH: 430 Senios acids
IEMPORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
                             TYPE: amino acid
TYPE: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: ONE MOUNTAIN CITY: FRAMINGHAM STATE: MASSACHUSETTS COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01701
                                                                                  4302 amino acids
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BURN, TIMOTHY C
CONNORS, TIMOTHY D
                                                                                                                                                                                                                     GEN4-17.8
                                                                                                                                                                                                                                                                                                                                                                                              Version
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Query Match
Best Local Similarity Conservative 5.3%; Score 84.5; 21.1%; Pred. No. 26; 35; Mismatches DB Length 4302; Indels Gaps

9

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; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-460-751-2

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                                                      Query Match
Best Local
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                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/460,751
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
CRISTION DATA:
APPLICATION NUMBER: US 08/413,580
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
ANALY: CRISTIA TAILED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                  TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reeders, Stephen
APPLICANT: Schneider, Michael
APPLICANT: Glucksmann, Sandra
TITLE OF INVENTION: IDENTIFICATION OF POLYCYSTIC KIDNEY
TITLE OF INVENTION: DISEASE GENE, DIAGNOSTICS AND TREATMENT
                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1600 -- TFRSVGTFNIIVTAE-----NEVGSAQDSIFVYV 1628
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                                                                                                                                                                                           TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 HTVFEHIHLLNETIIADEFATGPLGLNELKHLSRSISRWV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 QGLCDVLGGDASYGHRITKNPLSTAHATL-------WGPADALYELRALAHTLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
COUNTRY: U.S.A.
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  4 FETLFPESWLPRKPLASAEKSGAYRHV--
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                                      Similarity 21.1
59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     Coruzzi, Laura A.
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                                                        5.3%;
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                                                      Score 84.5;
Pred. No. 26;
                                      Mismatches 111;
-----TRQRALELPYIEANPLVMQSLVI 53
                                                                          DB 2;
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                                      Indels
                                      75;
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; SEQ ID NO 2; LENGTH: 450; TYPE: PRT; ORGANISM: Streptococcus pneumoniae US-09-191-879-2
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APPLICANT: Chalker, Alison F.
APPLICANT: Chalker, Alison F.
APPLICANT: Mazulla, Marie J.
TITLE OF INVENTION: DnaB
FILE REFERENCE: GM10183
CURRENT APPLICATION NUMBER: US/09/191,879
CURRENT FILING DATE: 1998-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09191879 Patent No. 6204014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.2%; Score 83.5; DB 4; Best Local Similarity 22.2%; Pred. No. 0.97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jaworski, Deborah APPLICANT: Wang, Min APPLICANT: Warren, Richard L. APPLICANT: Lennox, Anna L. APPLICANT: Ingraham, Karen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 7 SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: May, Earl
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                                           210
274 OKYTIAQGNLANASIYIDD--TPGIRITEIRSRSRKLAQ 310
                                                                                                                                                                               155 NRSGFKNIRDVLNLNFGNLEARSQQTTDITGIATGYRDLDHMTTGLHEEELIILAARPAV 214
                                                                                                                                                                                                                          124 ASYGHRITKNPLSTAHATLWGPADALYEL-----RALAHTLDEIH------ALPEA 168
                                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                                                                                                     82 TTTGHIVYALKNPVCLTDAARRRPI------NLLARVEQGLCDVLGGD 123
                                                                                                                                                                                                                                                                                                                                                                37 YIESRDFFKYAHRLIFQAMVDLSDRGDAIDATTVRTILDNQGDLQNIGGLSYLVEIVNSV 96
                                                                                                                                                                                                                                                                                                                                                                                                            40 YIE-----ANPLYMOSLV-ITDR-DASDA-----DWAADLAGLPSPSYV--SMNRV 81
                                        EHTVFEHIHLLNETTIADEFATGPLGLNELKHLSRSISR 248
                                                                                    GKTAFALNIAQNI-GTKLDKTVAIFSLEMGAESLVDRMLAAEGLVESHSIRTGQLTDEEW 273
                                                                                                                                 G-----NPRRNVTRSTVGRNVTLFD-----TTRMWAYRAVRHSWG---GPVA--EW 209
                                                                                                                                                                                                                                                                        PTSANAEYYAK - - IVAEKAMLRRLIAKLTESVNQAYEASQPADEIIAQAEKGLIDVSENA 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VNASRTVVPLNGSVSFSTSLEAGSDVRYSWVLCDRCTPIPGGPTISY- 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            43; Mismatches
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US-08-928-361B-30
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Best Local S
Matches 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650-324-1678 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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REGISTATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 481
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3
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   859
                                                             257
                                                                                                                                                                                              202
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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mes 74; Conserv
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                                                      ETFRARQKAISLRGASKG-----GKEGGHKGGIASGASRRAHTRQQFLEGLS 303
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5 Sherman Avenue, Suite 6
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PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,

THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS

FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
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Pred. No. 3.
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LENGTH: 1721
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Best Local
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CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, C
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF
TITLE OF INVENTION: INFECTIONS
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SOFTWARE: PatentIn Ver
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                          COUNTRY: USA
ZIP: 94306-1840
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Patentin Release #1.0, Version #1.30
                                                                                                                                                                        PETERS, VERNY, JONES & BIKSA
S Sherman Avenue, Suite 6
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Pred. No. 8;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B

FILING DATE:

12-SEP-1997

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REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 650.324-676
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COMPUTER READABLE FORM:
MEDITM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1130 VVPDEEAKDQADKGKDGLIVPPTNSINKDPVTNTQYSNTTGNIINPETGKVIPGSLPGSL 1189
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APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                              APPLICANT: HERR, JOHN C.
APPLICANT: WRIGHT, RICHARD M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1336 ET-----GDKLQGSHSGTFMPVPGKPQGENGGIM-----TPEQILEALN 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1238 -GDEIL-TEVLNITTDEVTGLPIDLETGLPRDPVSGLPQLPNGTLVDPSNK---KPIPGS 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1190 NYPSENTPQQTDEITGKPVDTVTG------LPYDPSTGEIIDPATKLPIPGSVA---- 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 PADALYELRALAHTLDEIHALP---EAGNPRRNVTRSTVGRNVTLFDTTRMWAYRAVRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 ETFRARQKAISLRGASKG-----GKEGGHKGGIASGASRRAHTRQQFLEGLS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 WGGPVAEWEHTVFEHIHLLNETIIADEFATG-PL----GLNELKHLSRSISRWVWRNFTP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 25.3 hes 74; Conservative
                                                                                                                                         COUNTRY:
                                                                                                                                                              CITY: Arlington STATE: Virginia
                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 -YALKNPYCLTDAARRRPINLLARVEQGLCDVLGGDASYGHRI---TKNPLSTAHATLWG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 VITDRDASD-ADWAADLAGLPSPSYVSMNRVT-----TTGHIV------
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TOPOLOGY: linear
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                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                    E: P.C.
1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                            U.S.A.
                                                                                                                                                                                                                                            OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.2%;
25.3%;
                                                                                                                                                                                                                                                                                      PRIMATE INTRA-ACROSOMAL SPERM ANTIGEN FOR USE IN A CONTRACEPTIVE VACCINE 29
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Pred. No. 8;
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                      Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
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RESULT 8
US-09-031-485-33
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Best Local S
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              APPLICANT: Tang, Liang
APPLICANT: Blebm, E. Scot
APPLICANT: Blebm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 03-MAR-198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GEHLSGEQSLG-EHASG 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 -IHLLNETIIADEFATG 232
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                                                                                                                                                                                                                                  STREET: 1825 SHALP
CITY: Fort Collins
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CLASSIFICATION: 530
                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Oblon, No. 5602005man REGISTRATION NUMBER: 24,618
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                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                   ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation
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                                                                                                                                                                                                                                                               E: Heska Corporation
1825 Sharp Point Drive
                                                                                                                                                                                                          USA
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(703) 413-2220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.2%; Score 83; DB 1; Length 285; 29.9%; Pred. No. 0.54;
                                                     US/09/031,485
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1989
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                                                                                            Version
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-031-485-33
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Best Local Similarity
"---hes 79; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-847-429A-33
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 33, Application US/08847429A Patent No. 5827692 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1653
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1445 ALEVPDIDIRQVRHQLVGLEAVTILRIWIFLKKEQATPVALRSALQRIGRDDVVR-EMDR 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1385 AITLPEYTGPEPMYSKKLFYSEASLTEKYVGAFHETAEPDNLPLAHVALLIGADWHRLAR 1444
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LENGTH: 1745 amino aci
                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                     TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
                                                                                                                                                                                STREET: 1825 Sharp Point Drive CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 ALELP-YIEANPLYMQSLYITDRDASD-----------ADWAADLA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/847,429 FILING DATE: 24-APR-1997
                                                                                                                                                                                                                 ADDRESSEE: Heska Corporation
                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --EQQETSKEGTFGCQTTHEKEKDDDGGSLKTTMKDSHVRQIFFDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLPSP-----SYVSMNRVTTTGHIVYALK---NPVCLTDAARRRPINLLARVEQGL 116
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)GY: linear
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 NUMBER:
                                                                                                                                                                                                                                      Carol Talkington Verser,
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US/08/847,429A
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Pred. No. 3
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US-09-065-474-33
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Best Local
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                                                                                                                                            COUNTRY:
                                                                                                                                                                                                STREET:
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US-08-847-429A-33
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APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 33:
                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1445 ALEVPDIDIRQVRHQLVGLEAVTILRIWIFLKKEQATPVALRSALQRIGRDDVVR-EMDR 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1385 AITLPEYTGPEPMVSKKLFYSEASLTEKYVGAFHETAEPDNLPLAHVALLIGADWHRLAR 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1504 AEKLDG------LEGTPVS--HIS--GPS-----ITLSSTLLEV-----AGDRRRHAE 1541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 RARQKAISLRGA----SKGGKEGGHKGGIASGASRRAHTRQQFLEG
                                                                                                                                                                                                   CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 ALELP-YIEANPLYMQSLVITDRDASD------------ADWAADLA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGPVAEWEHTV---FEHIHLLNETIIADEFATGPLGLNELKHLSRSISRWVWRNFTPETF
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                                                                                                                                                       80525
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6063599
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                                                                                                                                                                                                                                               1825 Sharp Point Drive
                                                                                                                                                                                 USA
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22.8%; Pred. No. 3
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US/09/065,474
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                                            Version
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24-APR-1998

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.9%;
Best Local Similarity 22.8%;
Matches 79; Conservative 31
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Randazzo,
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
                                                                        MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1385 AITLPEYTGPEPMYSKKLFYSEASLTEKYVGAFHETAEPDNLPLAHVALLIGADWHRLAR 1444
                                                                                                                                                                  MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1745 amino aci
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1653 -- EQQETSKEGTFGCQTTHEKEKDDDGGSLKTTMKDSHVRQIFFDG 1696
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2
CLASSIFICATION:
                   CLASSIFICATION:
                                           FILING DATE:
                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 94608-2916
                                                                                                                                                                                                                                                     CITY: Emeryville
STATE: California
                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 GLPSP-----SYVSMNRVTTTGHIVYALK---NPVCLTDAARRRPINLLARVEQGL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 ALELP-YIEANPLYMQSLVITDRDASD-----------ADWAADLA 68
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                                                                                                                                                                                                                                                                                             4560 Horton Street
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                                                                                                                                                                                                                                                                                                                                                                                                  Randazzo,
                                                                                                                                                                                                                                                                                                                     Chiron Corporation
                                     31-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                              Mammalian Deep
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                                                                                                                                                                                                                                                                                                                                                                                                  Filippo M.
                                                           US/08/904,452
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3:
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                            Orange Proteins
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RESULT: 12
US-08-683-908-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (510) 923-2718
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
TELEFAX: (212) 382-2124 INFORMATION FOR SEQ ID NO:
                                                                                                                             APPLICATION NUMBER: US/08/683,908
FILING DATE: 19-7UL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185626/1995
FILING DATE: 21-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                SOFTWARE: MS-DOS Editor CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 768-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Shimizu, Sakayu
APPLICANT: Kobayashi, Michihiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 -- FRPLYVLNEEGGPAPVCSLEAERGPDGRGFVI-ATTRQRLFQFI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 HTLDEIHALPEAGNP----RRNVTRSTVGRNVTLFDTTRMWAYRAV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 RVEQGLCDVLGGDASYGHRITKNP------LSTAHATLWGPADALYELRALA 156
                                                                         NAME: Davidson, Clifford M
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 3821004
                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U. ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                            CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 IDLGKASEPNRVELGRKDDAKVHKMFLDHTGSHLLVALSSTEVLYMNRNGQKARP---LA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 ADLAGLESPSYVSMNRVT-----TTGHIVYALKNPVCL---TDAARRRPINLLA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 QTGCPSVGIPHSGYVSAHLEKEVPIFTKQRVDFTPSERITSLVVSCNQLCMSLGKDTLLR 78
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RWKGQLVESVGWNKAMGNESSTGPILVGTAQGQIFEAELSASEGGLFGPAPDLY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                    New York
                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Steinberg, Raskin & Davi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     973 amino acids
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IBM PC compatible
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21.7%; Pred. No. 13;
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Expression of Nitrilase Gene,
                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
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US-08-342-930-2
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Best Local Similarity
                                INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1711 amino acids
                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 2034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: OLMSTE
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
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LENGTH: 1/11

mvpe: amino acid

ninear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 ATDAGDLAEVASLHNSAVDLLSAAIRT----ELADQAAASDGLLE----CVLAYIRQNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 YDILFPTDWRMSVFQFPRYSFGFTED-----FIGRMTAVNVGGDRGIGRVVSSFMTSIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 DPNLCASQIAAEHNVS---VRTLHRLFSATGQGVAEHIRNLR-----LERIKT--ELADP
                                                                                          TELEPHONE: (415) 494-0792
                                                                                      TELEFAX: (415
TELEX: 706141
                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/342,930 FILING DATE: 21-NOV-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 319 AMINO ACID RESIDUES
TYPE: AMINO ACID
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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DAVIS, ALAN R.
DIXON, JACK E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  755 Page Mill Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.8%; Score 77; DB 2; Length 319; 21.3%; Pred. No. 3; rative 33; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHATASE
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                                                                                                                                                                                                                                                                                                                Version #1.30
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                                                                                                                                                                                                                                                                 ; ORGANISM: Sorangium cellulosum US-09-413-814-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-413-814-42
                                                                                                                                                              Query Match
Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 42
LENGTH: 2539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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Patent No. 6225064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dougherty, Brian APPLICANT: Goldberg, Steven APPLICANT: Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cino, Paul M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Beyer, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gesellschaft fuer Biotechnologische Forschung APPLICANT: Bristol-Myers Squibb, Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mueller, Joachim
                                                                                                                                                                                                                                                                                                         TYPE: PRT
1629 ALCIPQQYPHLETSHVDLGVVHADELHAARQLDSLLAECLSATAERQLALRGRHRWLLDY 1688
                                                                                  1586 HLVQA----
                                 146 ADAL---YELRALAHT------ 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    638 --TLWGSERSSSANATGWTPPSAPTLVNVTSDAPTQLQVSWAHVPGGRSRY--QVTLYQE 693
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                                                                              Local Similarity nes 42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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                                                                                                                                                              Conservative
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                                                                                                                                                                               4.8%;
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                                                                                                                                                                               Score 77; DB 4; Length 2539; Pred. No. 78;
                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthesis of polyketide
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NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 3739
TYPE: PRT
ORGANISM: Streptomyces venezuelae
US-09-320-878-2
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EARLIER APPLICATION NUMBER: CIP OF 09/141,908

EARLIER APPLICATION NUMBER: CIP OF 09/141,908

EARLIER FILING DATE: 1998-08-28

EARLIER FILING DATE: 1998-08-28

EARLIER APPLICATION NUMBER: CIP OF 09/073,538

EARLIER APPLICATION NUMBER: CIP OF 09/073,538

EARLIER APPLICATION NUMBER: CIP OF 08/846,247

EARLIER APPLICATION NUMBER: 60/119,139

EARLIER FILING DATE: 1997-04-30

EARLIER FILING DATE: 1999-02-08

EARLIER APPLICATION NUMBER: 60/10,880

EARLIER APPLICATION NUMBER: 60/087,080

EARLIER APPLICATION NUMBER: 60/087,080

EARLIER APPLICATION NUMBER: 60/087,080

EARLIER FILING DATE: 1998-05-28

NUMBER: 60 STO 10 NOS-28
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US-09-320-878-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.8%; Score 77; DB 3; Length 3739; Best Local Similarity 22.3%; Pred. No. 1.4e+02; Matches 82; Conservative 23; Mismatches 100; Indels 162; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: McDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1723 AEHLARTTS 1731
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                                                     680 AARV----
                                                                                                                                                                                                                                                                                                                                                                529 AGGRAEFEHRAV--VLGT-----GODDFAQALTA------PEGLIRGTP----- 564
                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                     624 APTLERVDVVQPVTFAVMVSLAKVWQHHGVTPQAVVGH----SQGEIAAAYVAGALTLDD 679
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                                                                                                239 LKHLSRSISRWVWRNFTPETFRARQKAISLRGASKGGKEGGHKGGIASGASRRAHTRQQF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 LPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCD------V 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 LPRKPLASAEKSGAYRHVTRQR---ALELPYIEANPLVMQSLVITDRDASDADWAADLAG 69
                                                                                                                                                                                                             GPVAE-----
                                                                                                                                                                                                                                                                                                             RSTVGR------NVTLFDTTRM-----
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  --LEGLS
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303
                                                ----VTLRSKSIAAHLAG------KGGMISLALSEEATRQRI 715
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Search completed: October 4, 2002, 15:33:40 Job time: 32 sec



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Result
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Sequence 4, Appli	4	4	Sequence 7, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 2, Appli	•		5,	Sequence 52, Appl	•	Sequence 2, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 3, Appli

ALIGNMENTS

RESULT

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PATEMATION UNMERS: C. APPLICANT: Patison, James C. APPLICANT: Wen, Xiaohong APPLICANT: Gillespie, William APPLICANT: Gillespie, William APPLICANT: Medalhradszky, Katalin APPLICANTON MEDALSZ COUNTRY: Los Angeles STATE: CA ADDRESSEE: Poms, Smith, Lande & Rose STATE: CA COUNTRY: USA ZIF: 90067 COUNTRY: U	

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Patent No. 5962294
                                                                                                                          Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (310)788-5000
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 04-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 04-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/925369
FILING DATE: 04-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                      TOPOLOGY: 11
MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1:0, Version #1.25
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                                             52 SNRAEVVINGSSLPAVANRSNESLKHSIQPASSKW----
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REFERENCE/DOCKET NUMBER: 97
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                                                                          2 TTRERLPRNGYSIAAAAKKLGVS-----ESTVKRWTSEPREEFVARVAARHARIRELRSE 56
GQSMRAIAAEVGVSV--GT-----VHYALNKNRT 83
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Gillespie, William
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                                                                                                                          16.1%; Score 67.5; DB 2; Length 375; 25.3%; Pred. No. 0:75;
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                                                                                                                                                         US-08-494-907-20
                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Appropriate Patent No. 597
                                                                                                        Patent No. 5955298
GENERAL INFORMATION:
                                                                                                                          Patent No. 5955298
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 KQILKFLNAEKNISVLKGTLKPGNIIHYIFNRNST 132
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Versic
CURRENT APPLICATION NUMBER: US/08/956,012
APPLICATION NUMBER: US/08/956,012
FILLING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
APPLICANT: Weller, David APPLICANT: Cook, R. James
APPLICANT: Cook, R. James
TITLE OF INVENTION: Sequences for Production of
TITLE OF INVENTION: 2,4-Diacetylphloroglucinol and Methods
TITLE OF SERGIENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HUMAN HYDROXYPYRUVATE REDUCTASE NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                         APPLICANT: Thomashow, Linda S
APPLICANT: Bangera, Mahalaxmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hillman, Jennifer
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
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annual and Aporter Dr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                  DAAGANLKVIST---MSVGIDHLALDE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLPRNGYSIAAAAKKLGVSESTVKRWTSE---PREEFVARVAARHARI-----
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5972660
                                                                                                                                                                                                                           Application US/08494907
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                                                                                                                  Bangera, Mahalaxmi
Weller, David M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650-845-4166
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PCT-US96-10986-20
Sequence 20, Application PC/TUS9610986
GENERAL INFORMATION:
TITLE OF INVENTION: Sequences for 1
TITLE OF INVENTION: 2,4-Diacetylph.
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APPLICATION:
FILING DATE:
CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pendorf, Stephan A.
REGISTRATION NUMBER: 32665
REFERENCE/DOCKET NUMBER: A700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 14.6%; Score 61.5; DB 2; Length 130; Best Local Similarity 21.9%; Pred. No. 1.1; Matches 21; Conservative 11; Mismatches 25; Indels 3
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INFORMATION FOR SEQ ID NO:
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COMMUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Stephan A. Pendorf, DOMINIK & STEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acid
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NAME: Connor, Margaret A
REGISTRATION NUMBER: 3004
REFERENCE/DOCKET NUMBER:
                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
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MEDIUM TYPE: Floppy disk
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STREET:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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)GY: linear
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800 Buchanan Street
                                                                                                                                                                                                                                                                                                                USA
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US-08-494-907-16
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                                Matches
                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
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TELEFAX: (813)289-2967
INFORMATION FOR SEQ ID NO: 20
                                                                                                                                                                                                               TELEFAX: (510) 559-577 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Thomas
APPLICANT: Banger
APPLICANT: Weller
APPLICANT: Cook,
                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Connor, Margaret A
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                       LENGTH: 202 amino
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 800 B
CITY: Albany
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
10 NGYSIAAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELRSE------
                                                                                                                                                                                                                                                                                             NAME: Connor, Margaret REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                Conservative
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Weller, David M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thomashow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Margaret A. Connor, USDA-ARS
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                                               14.6%;
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                             ; Score 61.5; I
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11; Mismatches
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PCT-US96-10986-16
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; MOLECULE TYPE:
PCT-US96-10986-16
                                                                                                                                                                                                                                            Sequence 12, Application US/08160524A Patent No. 5851761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (813)289-296 INFORMATION FOR SEQ ID NO:
                                                                                                         APPLICANT:
APPLICANT:
                           TITLE OF INVENTION: PROBES, KITS AND METHODS FOR THE TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF MYOCBACTERIA NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PATENTIA RELEASE #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10986
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephan A. Pendorf, DOMINIK & STEIN
     CORRESPONDENCE
                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      88 NLNFLLLNLWKVWRETICGEAFRCVIAEAQLDPSTL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 NGYSIAAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELRSE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Pendorf, Stephan A. REGISTRATION NUMBER: 3266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Tampa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Stephan A. Fenduri, Dominion STREET: 600 N. West Shore Boulevard, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGLSIEAVARRAGASKPTIYRWWGNK-----AALIAEVYESESEQIRKEPDKGSFKE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGLSIEAVARRAGASKPTIYRWWGNK-----AALIAEVYESESEQIRKEPDKGSFKE 87
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(813)289-2967
                                                                                                         Catty, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 amino acids
                                                                                                                                Dale, Jeremy W.
Zainuddin, Zain
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                                                                                                                                                                                       McAdam, Ruth Anne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GOSMRAIAAEVGVSVGTV 74
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                                                                                                                                   Zainul Fadziruddin B.
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Pred. No. 2;
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A700.320
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US-08-473-020A-26
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INFORMATION FOR SEQ ID NO:
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FILING DATE: 18-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 890
FILING DATE: 22-FEB-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                     APPLICANT: Gicquel, Brigitte TITLE OF INVENTION: decide TITLE OF INVENTION: application of INVENTION: application of INVENTION: application of INVENTION: application of Invention of Inven
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CITY: San Francisco
STATE: California
"mited Stat
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LENGTH: 100 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: GB 9
FILING DATE: 09-JAN-1990
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 01-DEC-199
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MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
                           CORRESPONDENCE ADDRESS:
                                                    UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 MRAIAAEVGVSVGTVHYA 77
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les 18; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                     6, Application US/08473020A 5877273
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E: Attn: Walter H. Dreger
4 Embarcadero Center, Suite 3400
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                                                                                                                                                                                                                                                                Hance, Allan J
                                                                                                                                                                                                                                    Grandchamp-Desraux, Bernard
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                                                                                                                                                                                                           Levy-Frebault, Veronique
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23.1%; Pred. No. 0.88;
                                                    application
                                                                                                 applications to the synthesis or detection of nucleic acids, products of expression of such sequences and
                                                                                                                                                         Nucleotide sequences of actinomycetales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB 8903968.9
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Indels

12;

Gaps

2

4 Embarcadero Center, Suite 3400

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RESULT 10
US-08-491-357-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/623,729
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H
REGISTRATION NUMBER: 24190
REFERENCE/DOCKET NUMBER: A54435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO:
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   APPLICANT: Law, Susan
APPLICANT: Estojak, Joanne
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING A SIGNAL
TITLE OF INVENTION: MEDIATOR PROTEIN THAT INDUCES CELLULAR MORPHOLOGICAL
TITLE OF INVENTION: ALTERATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                              STREET: 1601 Market
CITY: Philadelphia
                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/473,020A FILING DATE: 06-JUN-1995
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                                                                                                                                                              COUNTRY:
APPLICATION NUMBER:
                                                                                                                                             ZIP:
                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 ERLPRNGY-SIAAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELRSEGQSMRAI 63
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                                                                                                                                           19103-2307
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                                                                                                                                                                                                                       E: Dann, Dorfman, Herrell and Skillman
1601 Market Street Suite 720
                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                           Golemis, Erica A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
US/08/491,357
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RESULT 11
US-08-968-633-3
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                                                                                            ATTORREY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
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Best Local Similarity 34.5
Matches 19; Conservative
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TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Golemis, Erica A.
APPLICANT: Law, Susan
APPLICANT: Estojak, Johnne
TITLE OF INVENTION: MUCLEIC ACID MOLECULE ENCODING A SIGNAL
TITLE OF INVENTION: MEDIATOR PROTEIN THAT INDUCES CELLULAR MORPHOLOGICAL
TITLE OF INVENTION: ALTERATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
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LENGTH: 872 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                493 RSTSEPQEPPVQDLKAAVAAVHGAVHELLEFARS--AVSSATHTSDRTLHAKLSR 545
                                                          LENGTH:
TYPE: a
          TYPE: amino acid
STRANDEDNESS: No. 6100384 Relevant
TOPOLOGY: No. 6100384 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720 CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: not rei
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                           872 amino acids
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protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.3%; Score 60; DB 1; Length 872; 34.5%; Pred. No. 23;
                                                                                                                                                                                                                                                                                          US/08/491,357
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; ANTI-SENSE: 1
US-08-968-633-3
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US-09-196-466-3
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RESULT 13
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GENERAL INFORMATION:
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Best Local Similarity 34.5
Matches 19; Conservative
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                           Matches
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ZIP: 19103-230,
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                     493 RSTSEPQEPPVQDLKAAVAAVHGAVHELLEFARS--AVSSATHTSDRTLHAKLSR 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493 RSTSEPQEPPVQDLKAAVAAVHGAVHELLEFARS--AVSSATHTSDRTLHAKLSR 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1001
CITY: Philadelphia
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                                                                                                                                            30 RWTSEPRE----EFVARVAARHARIRELRSEGQSMRAIAAEVGVSVGTVHYALNK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                              19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Law, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not relevant
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Th NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEIC ACID MOLECULE ENCODING A SIGNAL MEDIATOR PROTEIN THAT INDUCES CELLULAR
                                                                                                                                                                                                        14.3%; Score 60; DB 34.5%; Pred. No. 23; tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08/491,357
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Pred. No.
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                                                                                                                                                                                                                                                                    DB 3; Length 872;
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RESULT 14
US-09-071-434-1
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                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09071434 Patent No. 6080848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Sven, H
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 3:
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APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION UNMER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 872 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US96/10823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Estojak, JOAnne TITLE OF INVENTION: MUCLEZIC TITLE OF INVENTION: MEDIATO TITLE OF INVENTION: ALTERAT NUMBER OF SEQUENCES: 4
                                                                                                                                         APPLICANT: Corley, Neil C.
APPLICANT: Baughn, Mariah
TITLE OF INVENTION: HUMAN BRAIN-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
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                                                                                                                      CORRESPONDENCE ADDRESS
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                493 RSTSEPQEPPVQDLKAAVAAVHGAVHELLEFARS--AVSSATHTSDRTLHAKLSR 545
                  COUNTRY: UZIP: 94304
                                                     CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                               30 RWTSEPRE----EFVARVAARHARIRELRSEGQSMRAIAAEVGVSVGTVHYALNK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 19; Conserv
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CLASSIFICATION:
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                                                                                       3174 Porter Dr
                                     USA
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                                                                                                       Incyte Pharmaceuticals, Inc
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Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:

FastSEQ for Windows Version 2.0

US/09/071,434

COMPUTER: IBM Compatible OPERATING SYSTEM: DOS

MEDIUM TYPE:

Diskette

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US-08-335-844A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.0%;
Best Local Similarity 31.9%;
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                                                                                                                                                                                                                                                                                                  APPLICANT: OLIVER, JOANNA JANE
APPLICANT: NEWTON, SUSAN ELIZABETH
TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
TITLE OF INVENTION: AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: BRAIN
CLONE: 662575
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 LSPLQVAEN 205
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                                                                                                                                                                                          CITY: Washington STATE: D. C.
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TOPOLOGY: lin
APPLICATION NUMBER: US/08/335,844A FILING DATE: 09-JAN-1995
                                                                                                                                                          ZIP:
                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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FILING DATE: Filed Herewith
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SMITH, TREVOR STANLEY
MUNN, EDWARD ALBERT
KNOX, DAVID PATRICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 11; Mismatches
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Best Local Similarity 28.1%;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 35,400
REFERENCE/DOCKET NUMBER: 11.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: GB 9: FILING DATE: 08-MAY-1992 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 977 amino acids
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                                                        24 SESTVKRWTSEPREEFVARVAARHARIRELRSEGQSMRAIAAEVGVSVGTVHYALNK 80 : : : : | : | : | : | : | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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3 AEESQEQETQQPRKNTVLRLTP----IKSL----FALLVVAAAVGLSIGLTYYFTRK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WALKER, Barbara W.
WALKER, Barbara W.
11
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(202)783-0031
(202)783-6031
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Gaps

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Search completed: October 4, 2002, 15:33:41
Job time: 33 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 200000000
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   SPTREMBL_19:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb):
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebra
14: sp_unclass:
15: sp_archeap
17: sp_archeap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           562222 seqs, 172994929 residues
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Gapop 10.0 , Gapext 0.5
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420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_bacteria:*
sp_fungi:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
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sp_rvirus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	80	7	σ	U	4	ω	N		Result No.
78	78	78	78	78	78	79	82	82.5	96	110	121	140	162	215	420	Score
18.6	18.6	18.6	18.6	18.6	18.6	18.8	19.5	19.6	22.9	26.2	28.8	33.3	38.6	51.2	100.0	Query Match Length DB
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Q9k393 streptomyce	Q9x467 streptomyce	Q9rju2 streptomyce	O86758 streptomyce	Q97zw9 sulfolobus	Q9ex03 streptomyce			_		O30682 rhodococcus	Q9f5n5 rhodococcus	Q9lbj5 rhodococcus	Q9f4v5 brevibacter	Q46076 corynebacte	Q9f6k0 propionibac	Description

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72.5 72.5 72.5 72 72	72.5 72.5 72.5 72.5	74 73.5 73 73 73 72.5	78 78 78 75 75 75 74 74 74 74 74 74
17.3 17.3 17.3 17.1 17.1	17.3 17.3 17.3 17.3		
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047801 enterococcu 093165 enterococcu 093np3 enterococcu 068709 yersinia pe 053005 escherichia 099qi0 caulobacter	7	Q92144 rhizobium m Q92144 rhizobium m Q85930 sphingomona Q98b11 rhizobium 1 Q88091 escherichia Q92336 rhizobium m Q9r915 rhizobium m	യയാറായ പ്രവ

ALIGNMENTS

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61 RAIAAEVGVSVGTVHYALNKNRTDA 85 	1 MTTRERLPRNGYSIAAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELRSEGQSM 60 	Query Match 100.0%; Score 420; DB 2; Length 85; Best Local Similarity 100.0%; Pred. No. 2.2e-35; Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 85 AA; 9425 MW; 30FBBA897F0CC6F0 CRC64;		Appl. Environ. Microbiol. 67:499-503(2001). EMBL; AF291751; AAG25295.1;	•	"Efficient transformation system for Propionibacterium freudenreichii		Jore J.P.M., van Luijk N., Luiten R.G.M., van der Werf M.J.,	MEDLINE=21091935; PubMed=11157209;	STRAIN=LMG16545;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=1744;			Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;	Plasmid p545.	Propionibacterium freudenreichii.	REP2.	19, Last	. (TrEMBLrel. 16,	-2001 (TrEMBLrel.	Q9F6KO;	Q9F6K0 PRELIMINARY; PRT; 85 AA.	KO	LT 1

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RESULT

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Best Local (
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Q9F4V5;
01-MAR-2001
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Q46076;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=1014;
Shi S.L., Wang Z.X., Deng Y., Zhu H., He B., Zheng Z.X.;
"Complete Nucleotide Sequence of a Plasmid pXZ10142 from Corynebacterium glutamicum.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; X72691; CAA51239.1;
                                                                                                                                                                                                                                                              "Nucleotide sequence of a plasmid from Brevibacterium l: "Nucleotide sequence of a plasmid from Brevibacterium l: Construction of a cloning vector.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases EMBL; AY004211; AAF89086.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales;
Corynebacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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MTAEHRHPRNGMSVRELAAKVGVSEKSIVRWTSEPREVYLSRAQQRRVRIRELRETGLS
                                          MTTRERLPRNGYSIAAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELRSEGQS 59
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(TrEMBLrel. 19, Last sequence up
(TrEMBLrel. 19, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Micrococcineae; Brevibacteriaceae; Brevibacterium.
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Last sequence update)
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Pred. No. 1.3e-14;
7; Mismatches 18
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                                                                                             Score 162; DB 2;
Pred. No. 2.3e-09;
7; Mismatches 20
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Q9LBJ5;
Q9LBJ5;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                           DNA-binding; Pu
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InterPro; IPR000792; HTH_LuxR.
DNA-binding; Plasmid.
SEQUENCE 93 AA; 10124 Max.
                                                                                                                                                                                                                                                      Ryabchenko L.E., Novikov A.D., Golyshin P.N., Yanenko A.S. "Rhodococcus erythropolis plasmid pN30 putative replicase putative DNA-binding replication protein (ORF2)."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF312210; AAG29855.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9F5N5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
purarive DNA-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-IFO3338;
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pN30
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RRKMTAAAAAEKFGASTRTIQRLFAEPRDDYLGRAKARRDKAVELRKQGLKYREIAEAME
                                            RNGYSIAAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELRSEGQSMRAIAAEVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
31; Conserv
                                                                                       Similarity 37.8
28; Conservative
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                                                                                                                                                                                                                10409 MW;
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                                                                                                               28.8%;
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Pred. No. 5.7e-07;
4; Mismatches 23;
                                                                                         Score 121; DB 2;
Pred. No. 4.9e-05;
4; Mismatches 32;
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"Structural analysis of the 6-kb cr Rhodococcus erythropolis NI86/21 an Rhodococcus shuttle vectors.";
Microbiology 143:3137-3147(1997).
EMBL, AF015088; AAC45811.1;
DNA-binding; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9L456;
01-OCT-2000
01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Propionibacterineae; Propionibacterium.

NCBI_TaxID=1749, 1748;
[1]
                                                                         SPECIES-P. jensenii; STRAIN-DF1;
Stierli M.P., Meile L., Teuber
"Molecular analysis of plasmid
Propionibacterium jensenii.";
                                                                                                                                                                                                                                                                                                                    Propionibacterium jensenii, and Propionibacterium acidipropionici Propionibacterium acidipropionici Plasmid pLMEIO6, and Plasmid pRGO
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STRAIN-N186/21;
MEDLINE-98015402; PubMed-9353918;
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Plasmid praJ3600.
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Corynebacterineae; No
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE DNA-BINDING REPLICATION PROTEIN.
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(TrembLrel. 15, Last sequence update)
(TrembLrel. 16, Last annotation update)
L 13.0 KDA PROTEIN (REPLICATION PROTEIN)
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llarity 35.7%;
Conservative 1
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Pred. No. 0.00063;
2; Mismatches 33;
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EMBL; AJ250233; CABB8397.1; -.
EMBL; AB007909; BAB17920.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 114 AA; 13048 MW;
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EMBL; X84655; CAA59149.1; ...
SEQUENCE 105 AA; 12317 MW; 295DD15830188041 CRC64;
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Yamashita M., Murooka Y.;
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(TIEMBLIE1. 01, Last sequence update)
(TIEMBLIE1. 19, Last annotation updat, 13.7 KDA PROTEIN.
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HYPOTHETICAL

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Q93Q22;
Q1-DEC-2001
Q1-DEC-2001
Q1-DEC-2001
                                                                                           Q9EXO3 PRELIMINARY; PRT; 132 AA.
Q9EXO3; O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL (TrEMBLR)
AYPOTHETICAL (TREMBLR)
2SCG38.16.
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Hypothetical protein; Plasmi
SEQUENCE 119 AA; 13687 Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Yuen K.Y., Woo P.C.Y., Leung P.K.L.;
"Insertion sequence of Burkholderia pseudomallei.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF287634; AAK58883.1;
SEQUENCE 87 AA; 10211 MW; 69505094D5308D0E CRC64;
    Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; St
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Bacteria; Proteobacteria; beta subdivision; Burkholderia
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Rauzier J., Moniz-Pereira J., Gicquel-Sanzey
"Complete nucleotide sequence of pAL5000, a p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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NCBI_TaxID=1766;
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Plasmid pAL5000
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19; Conserv
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26; Conser
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nilarity 36.1%;
Conservative
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119 AA; 13683 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 79; DB
Pred. No. 0.81
9; Mismatches
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1.57;
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ERLPRNGYSIAAAAKKLGVSESTVKRWTSEPREEFVARVA-ARHARIRELRSEGQSMRAI 63

Matches Query Match Best Local

Similarity

18.6%; 28.6%;

Conservative

17;

37;

Indels

6,

Gaps

2

Length 150

Score 78; DB 1 Pred. No. 1.9; 17; Mismatches

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Best Local S
Matches 27
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G., Awayez M.J., Chan Weiher C.C.-Y., Clausen I.G., Curtis B.A., De Moors A., Erauso G., Fletcher C., Gordon P.M.K., Heikamp de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N. Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T., Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.; "The complete genome of the crenarchaeon Sulfolobus solfataricus Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

EMBL; AE006677; AAK40779.1; -
Hypothetical protein; Complete proteome.

150 AA; 17577 MW; E14E9250440E56B6 CRC64;
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Saunders D.C.
                                                                                                                                                                                                                Sulfolobus solfataricus Archaea; Crenarchaeota; NCBI_TaxID=2287;
                                                                                                                                                                                                                                                                                01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Redenbach M., Kieser H.M., Denapaite D., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed
                                                                                                                                                               STRAIN~ATCC 35092 / DSM 1617 / P2;
MEDLINE~21332296; PubMed~11427726;
                                                                                                                                                                                                                                                         SS00454
                                                                                                                                                                                                                                                                    HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL; AL445503; CAC13075.1; -.
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Cerdeno A.M.,
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Submitted (OCT-2000)
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SEQUENCE FROM
                                                                                                                                                                                          SEQUENCE FROM N.A.
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27; Conser
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                                                                                                                                                                                                                               Sulfolobales;
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e EMBL/GenBank/DDBJ databases.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                            Created)
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Pred. No. 1.6;
9; Mismatches
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                                                        solfataricus P2.";
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Best Local S
Matches 29
  Q9RJU2;
Q9RJU2;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TRANSPOSASE.
SC6A9.26 OR SCJ11.20.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1999) to the EMEREMBL; ALIO31035; CAAL19911.1; --
EMBL; ALIO9949; CAB52905.1; --
InterPro; IPRO01584; Rve.
Pfam; PF00665; rve; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Redenbach M., Kieser H.M., Denapaite D., Elcnner A Rinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the 8 Mb Streptomyces coelicolo Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkhill J., Barrell Submitted (JUL-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales;
NCBI_TaxID=1902;
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                                                                                                                                       AAAVEEHVLRLRREH-RIGPLR---
                                                                                                                                                                                  ----EEFVARVAARHARIRELRSEGOSMRAIAAEVGVSVGTVHYAL
                                                                                                                                                                                                                             TGRLRLARCVVEDGWPVRRAAERFQVSHTTASRWARRYRQLGVTGMSDRSSRPHHQPRRT
                                                                                                                                                                                                                                                            TTRERLPR----NGYSIAAAAKKLGVSESTVKRWT--
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(JUL-1998) to
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                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkhill J.,
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36530 MW;
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27.4%;
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e EMBL/GenBank/DDBJ
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e EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                        Score 78; DB Pred. No. 4.4; L1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases
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                       PRT;
                                                                                                                                     -----LAVRCGIAASTAHRIL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                       61446BB9CA1DBEE9
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                                                                                                                                                                                                                                                                          SEPR--
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RESULT
Q9X467
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Best Local :
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01-MAY-2000 (TIEMBLIGE).
01-JUN-2001 (TIEMBLIGE).
TRANSPOSASE (PUTATIVE IN
SCF41.27 OR SC10B8A.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; 1Photoproper Pfam; PF00665; r 918 /
                                                                                                                                                                      01-NOV-1999
01-NOV-1999
01-DEC-2001
                                                                                                                                                                                                                                   Q9X467;
                                                                                                                              TNPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-2000) to the EMBL; AL117387; CAB55730.1; EMBL; AL391454; CAC04115.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacterida
Bacteria; Firmicutes; Actinobacteria; Actinobacterida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thomson N.R.,
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Submitted (SEP-1999) 1
                                                                                   Bacteria;
                                                                                                     Streptomyces coelicolor.
                                                                                                                                                    TRANSPOSASE
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"A set of ordered cosmids and a detailed genetic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97000351; PubMed-8843436; Redenbach M., Kieser H.M., Denapaite D.,
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SEQUENCE FROM N.A.
                                                               Actinomycetales;
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Microbiol, 21:77-96(1996).
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                                                                                   Firmicutes; Actinobacteria; Actinobacteridae;
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TTEMBLrel. 13, Last sequence update)
(TTEMBLrel. 17, Last annotation update)
(PUTATIVE INSERTION ELEMENT TRANSPOSASE).
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                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                               Streptomycineae;
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36544 MW;
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27.4%;
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EMBL/GenBank/DDBJ databases.
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EMBL/GenBank/DDBJ databases
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Last sequence update)
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Pred. No. 4.4;
L1; Mismatches
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                                                          Streptomycetaceae;
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                                                          Streptomyces
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RX MEDLINE-99250253; PubMed=10231572;
RA Chung H.J., Kim E.J., Suh B., Choi J.H., Roe J.H.;
RA Chung H.J., Kim E.J., Suh B., Choi J.H., Roe J.H.;
RT Streptomyces for Fer-containing superoxide dismutase in Fulplicate genes for Fer-containing superoxide dismutase in Fulplicate genes for Fer-containing superoxide dismutase in Figure 231:87-93(1999).

RT Streptomyces coelicolor A3(2).";
RI Gene 231:87-93(1999).
DR EMBL; AF099014; AAD33127.1; -.
DR InterPro: IPRO01584; Rve.
DR Pfam; PF00665; rve; 1.
DR FIGHER FOR STORE ST
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Run
                                                                                         OM protein -
                                                                                       protein search, using sw model
                                              October 4, 2002, 15:34:40;
                                                                                                                                                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
Search time 55.08 Seconds (without alignments) 171.410 Million cell updates/sec
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Title: Perfect score: US-09-720-583A-3 420

Sequence: MTTRERLPRNGYSIAAAAKK.....EVGVSVGTVHYALNKNRTDA

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

747574 segs, 111073796 residues

Total number of hits satisfying chosen parameters:

747574

Minimum DB Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s summaries

Database A_Geneseq_032802:*

1: /SIDSI/gcgdata/h
2: /SIDSI/gcgdata/h
3: /SIDSI/gcgdata/h
4: /SIDSI/gcgdata/h
5: /SIDSI/gcgdata/h
6: /SIDSI/gcgdata/h
7: /SIDSI/gcgdata/h
8: /SIDSI/gcgdata/h 110: 111: 113: 114: 115: 116: 117: 119: 119: 1: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
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4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
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7: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
8: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
9: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
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10: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
11: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
12: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
14: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
15: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
16: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
18: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*
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27: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
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29: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
20: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11	10	9	8	7	6	տ	4	ω	2	1	Result No.
66	67	67	67	69.5	76	79	79	.79	82	420	Score
15.7	16.0	16.0	16.0	16.5	18.1	18.8	18.8	18.8	19.5	100.0	Query Match
214	927	279	98	316	314	314	314	314	314	85	% Query Match Length DB
22	22	22	22	21	13	14	13	13	18	21	i
AAU59374	AAE10133	AAU44478	AAG91658	AAB14150	AAR20991	AAR34544	AAR37873	AAR29623	AAW14834	AAY44637	ID
Propionibacterium	Streptomyces nours	Propionibacterium	C glutamicum prote	Bordetella pertuss	Protein "d" encode	Tet e gene product	Tet e gene product	Tet e gene product	Protein encoded by	Propionibacterium	Description

Novel human enzyme	2 AAU23556	S N	356 362		62	U1 #A
		22	328	14.8	62	- ω
A human hydroxyp		20	328		62	Ñ
zea mays protein	L AAG40789	21	227	14.8	60	14
mays		2 1	204	14.0	5 K	ט מ
eptococci		2 2	158		62	8
Putative P. abyssi		22	507	14.9	62.5	7
3		22	2169	15.0	63	σı
		21	284	15.0	63	UI
	L AAG20358	,21	279	15.0	63	34
Arabidopsis thalia		21	247	15.0	63	ω
đ		22	219	15.0	63	N
		21	953	15.1	ω	
		21	763	15.1	u	٥
		21	580	15.1	ω	9
Pseudomonas putida		21	573	15.1	w	ш
Human polypeptide		22	547	15.1	w	7
E. coli cellular		22	326		w	O
-		22	211	15.1	ω	OI
		19	186	15.1	ω	42
		19	186	15.1	63.5	23
		19	186	15.1	ω	N
Escherichia coli	AAW44288	19	186		w	_
o		19	186		w	ن
E. coli Cam operon	3 AAW30754	18	186	15.1	ω	Ψ
C glutamicum prote		22	98	15.1	w	æ
C glutamicum prote	AAG90746	22	98	15.1	ω	7
Novel human diagno		22	1100	15.2	64	16
Drosophila melanog	2 ABB68417	22	743		64	ū
Propionibacterium		22	162		64	14
Drosophila melanog	2 ABB64106	22	868		65	3
Propionipacterium	141000041		-	٠	00.0	

ALIGNMENTS

AAY44637 ID AAY4 RESULT AAY44637 standard; Protein; _ 85 A

7

07-APR-2000 (first entry)

AAY44637;

Propionibacterium LMG 16545 protein-2.

Propionibacterium LMG 16545; vector; plasmid; antigen; vaccine; nutritional factor; growth factor; clotting factor; antimicrobia hormone; vitamin B12; animal feed; lactic acid bacteria; foodst

Propionibacterium freudenreichii LMG 16545

W09967356-A2

29-DEC-1999

25-JUN-1999; 99WO-EP04416

25-JUN-1998; 98EP-0305033

(KONN) GIST-BROCADES BY.

Pouwels PH, Van Luijk N, Jore JPM, Luiten RGM;

WPI; 2000-136977/12. N-PSDB; AAZ49691.

Novel vectors containing Propionibacterium sequences, used to homologous or heterologous proteins ${\ \ }$ express

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW14834
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present amino acid sequence is encoded by the endogenous plasmid Propionibacterium LMG 16345 ORF-2, derived from propionibacterium freudenreichii deposited under CBS 101022 or CBS 101023. The vector has insertion sites for foreign DNA fragments and is capable of autonomous replication. It can be used safely as they remain extrachromosomal and are very stable. They can be used to express homologous or heterologous proteins, which may include antigens for use in veccines, nutritional, growth and clotting factors, antimicrobials, vitamins (especially vitamin B12), enzymes, hormones and drugs. The Propionibacterium host cells are used in the production of animal feeds, manufacture of foodstuffs like, sausages and cheese, where they may be used instead of or in addition to lactic acid bacteria and in the manufacture of vitamin B12. The DNA sequence can also be used as a source of primers and probes.
                                                              Mycobacteria expressing secretion signal of lipoprotein and heterologous antigen, esp. outer surface protein A or B of Borrelia burgdorferi - are used in the form of a live bacterial vaccines
                                                                                                                   WPI; 1997-042315/04.
N-PSDB; AAT64413.
                                                                                                                                                                                                                                                                                                                                                             surface protein.
                                                                                                                                                                                                                                                                                                                                                                           Plasmid pMV101; Mycobacteria; lipoprotein antigen; bacterial vaccine; Lyme disease;
                         Example 1;
                                                                                                                                                              Stover
                                                                                                                                                                                                                 17-NOV-1992;
21-OCT-1991;
                                                                                                                                                                                                                                                        21-OCT-1991;
                                                                                                                                                                                                                                                                                  10-DEC-1996
                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by M.rep ORF1 of plasmid pMV101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW14834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW14834 standard; Protein; 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Page
                                                                                                                                                                                      (MEDI-) MEDIMMUNE INC
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                       Fig 5; 122pp; English.
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                                                    disease
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91US-0780261.
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Pred. No. 3.2e-46;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                         secretion signal sequence;
Borrelia burgdorferi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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The sequences

given in AAW14834-36 are

proteins which

are encoded

þу

Query Match

18.8%;

Score

79; DB

13;

Length 314;

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RESULT
AAR29623
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Sequence
                                                           This sequence is the
                                                                                                                                                                                                       Method of inducing cytotoxic T-lymphocyte response - esp. expression products of transformed Mycobacterium are useful as vaccines against HIV, pertussis, malaria, influenza virus, herpes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytotoxic T-lymphocyte response; transformed Mycobacteria; BCG; Mycobacterium smegmatis; vaccine; cell mediated immunity; HIV; pertussis; malaria; influenza virus; CTL; herpes virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Dela Cruz V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEDI-) MEDIMMUNE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                    1992-433380/52.
DB; AAQ31727.
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                                                                                                                   Fig
   314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product from pMV101 - a deletion mutant of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Stover CK;
                                                                                                                      5; 86pp; English.
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                                                              tet e
                                                           gene encoded by
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Pred. No. 0.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                           plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
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RESULT
AAR34544
ID AAR3
XX
AC AAR3
AC AAR3
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DT 04-J
XX
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Best Local S
Matches 26
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Matches 26; Conser
                        04-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytotoxic T-lymphocyte response; transformed Mycobacteria; Mycobacterium smegmatis; vaccine; cell mediated immunity; pertussis; malaria; influenza virus; CTL; herpes virus.
                                                              AAR34544;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dela Cruz V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUN-1993 (first entry)
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                                                                                              AAR34544 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the tet e gene encoded by plasmid pMV101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 5; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tetanus vaccination - by provoking an immune response using transformed Mycobacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-433378/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tet e gene product from pMV101 - a deletion mutant of pYUB125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MEDI-) MEDIMMUNE INC.
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                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                 5
                                                                                                                                                                                                                        VH---YALNKNR 82
                                                                                                                                                                                                                                                        aegaritglserhvvrlvaqersenlaeqaarrerirayeddegeswpqtakmfgleldt 282
                                                                                                                                                                                                                                                                                 AAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELR-SEGQSMRAIAAEVGVSVGT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vkrlgyrarker 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VH---YALNKNR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aegaritglserhvvrlvaqersenlaeqaarrerirayeddegeswpqtakmfgleldt 282
                                                                                                                                                                                      vkrlgyrarker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELR-SEGQSMRAIAAEVGVSVGT
                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                            314 AA;
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 36.1%;
Conservative
                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stover CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91US-0711084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92WO-US05023
                                                                                                                                                                                      294
                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 314
                                                                                                                                                                                                                                                                                                                                                 18.8%;
                                                                                                314
                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                  Score 79;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Mismatches
                                                                                                Ā
                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 0.098;
                                                                                                                                                                                                                                                                                                                                                 0.098;
                                                                                                                                                                                                                                                                                                                                                                   DB 13;
                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                   Length 314;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                4;
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                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
AAR220991
AAR2
AC AAR:
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                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is the tet e gene product encoded by plasmid pMY101. When the nucleotide was decoded, the sequence in the specification was found to contain several deletions and insertions which upset the reading frame. Also many codons were found to encode amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expression vector for expressing protein or polypeptide in mycobacterium - conty DNA sequences encoding lipoprotein secretion signal and peptide heterologous to bacteria expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytotoxic T-lymphocyte response; transformed Mycobacteria; Mycobacterium smegmatis; vaccine; cell mediated immunity; pertussis; malaria; influenza virus; CTL; herpes virus.
                      09-JUL-1991;
                                                                                                                              Synthetic.
                                                                                                                                                                Polymerase resistance;
                                                                                                                                                                                                                    Protein "d"
                                                                                                                                                                                                                                                        03-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-152187/18.
N-PSDB; AAQ41316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stover CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tet e gene product from pMV101 - a deletion mutant of pYUB125.
                                                        06-FEB-1992
                                                                                          WO9201783-A
                                                                                                                                                                                                                                                                                            AAR20991;
                                                                                                                                                                                                                                                                                                                              AAR20991 standard; Protein; 314 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acids contrary to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 5; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusion protein of lipoprotein heterologous to bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09307897-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223
                                                                                                                                                                                                                                                                                                                                                                                                                    283 vkrlgyrarker 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELR-SEGQSMRAIAAEVGVSVGT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VH---YALNKNR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                          chain reaction; mycobacterial promoter; kanamycin;
; BCG; Bacille Calmette-Guerin; origin of replicati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 AA;
                                                                                                                                                                                                                    encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                      (first entry)
                      91WO-US04833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the universal genetic code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.8%;
                                                                                                                                                                                                                    by mycobacterial plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 79; DB 14
Pred. No. 0.098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 14;
                                                                                                                                                                                                                    PMV101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 314;
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Gaps

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasmid pyUB12 was constructed by ligating a 5kb Sau3 fragment from pAL5000 (contg. a replication origin from M.fortuitum) to BamHI-digested pJU566 (contg. an E.coll ori and kanamycin neomycin resistance sequences). A 2586bp HpaI-EcoRV fragment from pYUB12 (comprising the minimum sequence necessary for plasmid replication in BCG) was ligated to PVUII-digested pYUB8 to form pYUB53. (plasmid pYUB8 is a pBR322 deriv. which includes an E.coli replicon and a kanamycin resistance gene). Twelve restriction sites were removed by digesting pYUB53 with hati, EcoRV and PstI. To eliminate 792 bases of the (inactivated) tet gene, the plasmid was digested with NarI and the 6407bp gel purified fragment was religated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   circularised. The resulting plasmid was designated pMV101. The nucleotide sequence of plasmid pMV101 is printed in the specification but the copy quality is too poor to allow the sequence to be included on the GENESEQ nucleotide database. Three proteins are encoded by pMV101, i.e. the kanamycin resistance protein and proteins "d" and "e" encoded by the complementary strand. See also AAR20992 and AAR20993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA site-specific integration into Mycobacteria - useful as adjuvant in vaccines and as therapeutic agent for malaria, influenza, herpes and human immunodeficiency virus
(ULBR ) UNIV LIBRE BRUXELLES
                                21-DEC-1998;
                                                                 21-DEC-1999;
                                                                                                  29-JUN-2000
                                                                                                                                 WO200037493-A2
                                                                                                                                                                Bordetella pertussis
                                                                                                                                                                                                 Type III secretion system; virulence
                                                                                                                                                                                                                              Bordetella pertussis protein # 4.
                                                                                                                                                                                                                                                                    02-FEB-2001
                                                                                                                                                                                                                                                                                                                                 AAB14150 standard; Protein; 316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig 24; 82pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                   283 vkrlgyrarker 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 aegaritglserhvvrlvaqersewleaqaarrerirayhddeghswpqtakhfglhldt 282
                                                                                                                                                                                                                                                                                                                                                                                                                                        74 VH---YALNKNR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELR-SEGQSMRAIAAEVGVSVGT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WR, Hatfull G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EINSTEIN A COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90US-0553907
                                98GB-0028217.
                                                                 99WO-EP10297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 76; DB 13; Length 314; Pred. No. 0.24; 8; Mismatches 35; Indels
                                                                                                                                                                                               factor; pathogenicity island
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT
AAG91658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella pertussis possesses a type III secretion system. Type III secretion systems allow bacteria to target virulence factors directly at host cells. The present sequence is a protein of B. pertussis. No name has been specified for the present sequence. The coding sequence of the present sequence is homologous to housekeeping genes of other species, and so the present protein may have a role in cellular housekeeping. A pathogenicity island is a compact, distinct genetic unit carrying virulence genes. The coding sequence of the present sequence is located within a pathogenicity island (see AAA64890) which also carries, a number of genes encoding proteins involved in the type III secretion system of B. pertussis. See AAA64894-A64884 and AAB14111-B14146 for details of the coding sequences and proteins identified in the pathogenicity island, of the present invention.
                                                                                                16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                                  Nakagawa
Tateishi
                                                                                                                                                                                                                                                      Coryneform bacterium; a organic acid synthesis.
                                                                                                                                                                                                                                                                                         C glutamicum protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polypeptides derived from Bordetella pertussis, useful for treating and diagnosing Bordetella infection -
                                                                                                                                                                                                                            Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                      AAG91658 standard; Protein; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
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                                                                                                                                                  18-DEC-2000; 2000EP-0127688
                                                                                                                                                                             20-JUN-2001
                                                                                                                                                                                                     EP1108790-A2
                                                                                                                                                                                                                                                                                                                    26-SEP-2001
                                                                                                                                                                                                                                                                                                                                             AAG91658;
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                                                                        (KYOW ) KYOWA HAKKO KOGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                                                                                                                                                                                   88 tqariaqalgvsastvsrvl 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMRAIAAEVGVSVGTVHYAL
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                                   zο
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                                                                                                ; 99JP-0377484.
; 2000JP-0159162.
; 2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pages 160-161; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                   Mizoguchi H, Ar
Senoh A, Ikeda
                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                            glutamicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.5%;
                                                                                                                                                                                                                                                                                           fragment SEQ.ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P,
                                                                                                                                                                                                                                                                  amino
                                  Ando
eda M,
                                                                          Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                            78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                  acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 69.5;
Pred. No. 1
                                   S, Hayashi M,
Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                  synthesis; vitamin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ħ
                                                                                                                                                                                                                                                                                           5412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
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                                               Ochiai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 316;
                                                                                                                                                                                                                                                                   saccharide
                                               7
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                                                Yoko1
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WPI; 2001-376931/40 N-PSDB; AAH66877.

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RESULT
AAU44478
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a first identifying
          Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU44478 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                              Skeiky YAW,
                                                                                                                                                                                        07-JUL-2000;
                                                                                                                                                                                                     21-APR-2000;
02-JUN-2000;
                                                                                                                                                                                                                                               20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                                             01-NOV-2001
                                                                                                                                                                                                                                                                                                          WO200181581-A2
                                                                                                                                                                                                                                                                                                                                       Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                  dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                           SAPHO syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes immunogenic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU44478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                      N-PSDB;
                                                                                                               L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                              inflammatory
                                                                                                                                                          CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 gtsigkiandlginrmtlknwitkyganstphgantatalseaerirglekenallr 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 GYSIAAAKKLGVSESTVKRW-----TSEPREEFVARVAARHARIRELRSEGQSMR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                    2001-616774/71.
DB; AAS59522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                               endophthalmitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   point of a gene, measuring expression of a gene, analysing on profile or pattern of a gene and identifying homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO: 5412; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
                                                                                                                                                                                    ; 2000US-199047P.
; 2000US-208841P.
; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention provides a number
                                                                                                                             Persing DH,
                                                                                                                                                                                                                                                                                                                                                                             me; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
pphthalmitis; bone; joint; central nervous system; ELISA;
lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                 osteopathic;
                                                                                                               Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.0%;
                                                                                                               ۲,
                                                                                                              Mitcham JL, Wang SS,
, Jen S, Carter D;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                 neuroprotectant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 23
                                             16-AUG-2001
                                                                                                                                                                                                                                  Doma in
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                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE10133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE10133 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID No 5673; 1069pp;
                                                                                      WO200159126-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polyketide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthase; PKS; macrolide; nystatin; PKS gene cluster;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibiotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                      /label= TM2
/note= "Transmembrane
884..912
                                                                                                                                                                                                                            /label= TM1
/note= "Transmembrane domain"
583..610
                                                                                                                                                                                                                                                                                               /note= "Leucine 548..568
                                                                                                                                                                                                                                                                                                                                     /label- LZ
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                        'note= "LuxR-type helix-turn-helix motif (DNA binding)"
                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.0%; Score 36.5%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcriptional activator
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                                                                                                                                                                                         domain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
2.9;
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are used in
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08-FEB-2001; 2001WO-GB00509

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RESULT 11
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Best Local
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10-APR-2000;
14-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the cloning and sequencing of the cluster encoding a modular type I polykentase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antifungal antibiotics. The present sequence is a transcriptional activator encoding Streptomyces nour
                                                                   01-NOV-2001
                                                                                                                                                                                                   dermatological;
                                                                                                                                                                                                                 SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
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(SNTF)
(ALPH-)
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S, Ellingsen "
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SEKUROVA O N.
FJAERVIK E.
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DZIEGLEWSKA H.
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2000GB-0008786.
2000GB-0009387.
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Pred. No. 14;
                                                                                                                                                                                                   neuroprotectant.
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AAU58347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC pustulosis, hypertosis and osteomyelitis), uveltis and endophthalmitis.

CP acnes is also involved in infections of bone, joints and the central concrous system, however it is particularly involved in the inflammatory concrete the contraction of the central concrete the contraction of the sentence of lesions associated with acne vulgaris. A method for detecting the contacting a concrete that binds to the proteins of the invention of sample with a binding agent that binds to the proteins of the invention of an determining the amount of bound protein in the sample. The concrete considering the amount of bound protein in the sample of the invention of an antipolate sample of the proteins. The production of antibodies conspectifies for p. acnes proteins. These antibodies can be used to concretely attences and activity of p. acnes properties and concept treat p. acnes infections. The antibodies may also be used as consensuable agents for determining p. acnes presence, for example, by constitute agents for determining p. acnes presence, for example, by constitute agents for determining p. acnes presence, for example, by constitute the sequence data for this patent did not form part of the printed constitution, but was obtained in electronic format directly from MIPO can be the printed constitution of                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches 24
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02-JUN-2000;
07-JUL-2000;
                                                                                                            SAPHO syndrome; synovitis; acne; uveitis; endophthalmitis; bone; inflammatory lesion; acne vulgari
                                                                                      dermatological;
                                                                                                                                                                                                   Propionibacterium acnes immunogenic protein #19243.
                                                                                                                                                                                                                                                                                                   AAU58347;
                                                                                                                                                                                                                                                                                                                                               AAU58347 standard; Protein; 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAU39105-AAU68017 represent Propionibacterium acnes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L'maisonneuve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             lssnpq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt trsrkprspshglaslftmaklgvptssvpesetpkrwttspstshtaltnhadtakifd}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                90
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; 2000US-208841P.
; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                       ne; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
ophthalmitis; bone; joint; central nervous system; ELISA;
lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                 (first entry)
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e J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ă,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The proteins and their associated DNA sequences are used by prevention and diagnosis of medical conditions caused by
                                                                                    osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No 20569; 1069pp; English.
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, Carter D;
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                                                                                                                                                                                                      RESULT 13
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Best Local S
Matches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme linked immunosorbent assay (ELISA).
Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
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               pharmaceutical
                               Drosophila; developmental biology; cell signalling; insecticide;
                                                               Drosophila melanogaster polypeptide SEQ ID NO 19110
                                                                                                                                                                      ABB64106 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAU39105-AAU68017 represent Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID No 19542; 1069pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                        rereilrlaesgasisliaselclsvgtvrnhvssaigktgaanrtea
                                                                                                                                                                                                                                                                                                                      rpgy--lrramdagvagflvkdtpaedlaqvvrkvhaggraidpalaaeslieghnplsg
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                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                     (first entry)
                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                           15.6%;
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, Jen S, Carter
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invent of discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB3737-ABB372072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid genes from Drosophila and interactions -
                                                                                           SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 19110; 21pp + Sequence Listing; English.
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11-JUL-2000; 2000US-0614150
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                                                         Propionibacterium acnes
                                                                                dermatological;
                                                                                                                                           Propionibacterium acnes immunogenic protein #17620
                                                                                                                                                                                             AAU56724;
                                                                                                                                                                                                                   AAU56724 standard; Protein; 162
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                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                osteopathic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection reagent for detecting
                                                                                                                                                                                                                                                                                                                                                                                 15;
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Pred. No. 23;
15; Mismatches
                                                                                neuroprotectant
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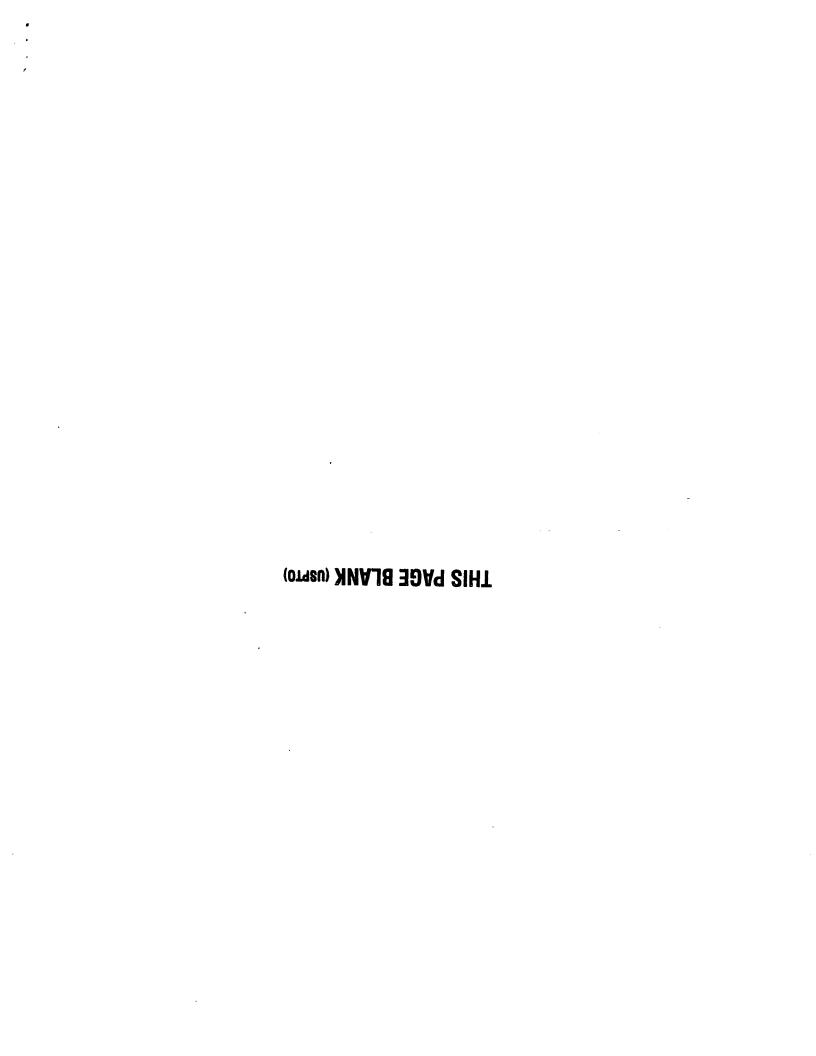
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyvlitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to therefore treat P. acnes infections. The antibodies can be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO cat fire, wipo.int/pub/published_pct_sequences.
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02-JUN-2000;
07-JUL-2000;
23-MAR-2001;
                                27-SEP-2001
                                                               WO200171042-A2
                                                                                                Drosophila melanogaster
                                                                                                                              pharmaceutical.
                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 32043
                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                ABB68417 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                              31 hrvsdvaallgvsddtvrrwidg------rhvraakdttgrlrvdgaslaa 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 17; Conserv
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; 2000US-208841P.
; 2000US-216747P.
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e J, Zhang '
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2001WO-US09231
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  Jen S, Carter D;
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Pred. No. 3.5;
9; Mismatches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                   sequences (ABL01840-
(ABB57737-ABB72072).
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ALIGNMENTS

C; Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7, Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C; Accession: AC2478
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, N.; Yamada, M.; Yasuda, M.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, N.; Yamada, M.; Yasuda, M.; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanoba A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanoba hypothetical protein 4 - Corynebacterium glutamicum
-C;Species: Corynebacterium glutamicum
-C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Jun-2000 A; Experimental source: C; Genetics: A; Molecule type: DNA A; Residues: 1-198 <KUR> A; Cross-references: GB: A;Reference number: AB1807; A;Accession: AC2478 A;Status: preliminary RESULT AC2478 밁 Š В Q A; Start codon: GTG C; Superfamily: Corynebacterium glutamicum hypothetical protein 4 C;Accession: S32702; S32200
R;Shi, S.L.; Wang, Z.X.; Deng, Y.; Zhu, H.; He, B.; Zheng, Z.X.
submitted to the EMBL Data Library, March 1993 A; Molecule type: DNA A; Residues: 1-105 <SHI> A; Reference number: \$32699 A; Accession: \$32702 transposase alr7003 [imported] - Anabaena sp. (strain PCC 7120) plasmid pCC7120alpha A; Cross-references: A; Status: preliminary A;Description: Complete nucleotide sequence of a plasmid pXZ10142 from Corynebacteriu Genetics: Matches Query Match Best Local 79 61 RAIAAEVGVSVGTVH 75 19 _ MTKRTRIPRNGKTIREVAEGTGLSTATIERWTSAPREDYLAQANEKRVRVQELRAKGLSM 78 MTTRERLPRNGYSIAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELRSEGQSM 60 40; Similarity Conservative GB:BA000020; PIDN:BAB78087.1; PID:g17135541; GSPDB:GN00180 ce: strain PCC 7120 EMBL: X72691 51.2%; Sequence of the Filamentous Nitrogen-fixing Cyanobacterium 7; MUID:21595285; PMID:11759840 93 ; Score 215; DI ; Pred. No. 7.8; 17; Mismatches DB 2; .8e-15; 18; Length 105 Indels 0; Yasuda, M.; Tabata Gaps A.; Irigu 0

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C;Accession: D90190

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awa:
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc,
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein SS00454 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 **sequence_revision 24-May-2001 **text_change 24-May-2001 **C;Date: 24-May-2001 **sequence_revision 24-May-2001 **text_change 24-May-2001 **change 24-May-2001 **sequence_revision 24-May-2001 **sequ
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Gene 71, 315-321, 1988
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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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A;Genome: plasmid
                                  A; Molecule type: DNA
A; Residues: 1-150 < KUR>
                                                                                                                               A; Reference number: A99139
A; Accession: D90190
                                                                                                                                                                                              A; Description: Sulfolobus solfataricus complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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A;Cross-references: GB:AE006641; NID:gl3813609;
                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical 13.7K protein - Mycobacterium fortuitum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 VKRLGYRARKER 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 NGYSIAAAAKKLGVSESTVKRW----TSEPREEFVARVAAR----HARIRELRSEGQSMRA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELR-SEGQSMRAIAAEVGVSVGT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNLSMIAEANKSPV----VPRFPQNTSLKRKVQSAKAQARRRDIHARVWSLRSIGLSVQA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEGARITGLSERHVVRLVAQERSEWLAEQAARRERIRAYHDDEGHSWPQTAKHFGLHLDT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VH---YALNKNR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAAEVGVSVGTVHYALNKN 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IAQSLGVAKNTVYNYLRSS 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moniz-Pereira,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            has a characteristic helix-turn-helix motif typical of DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.6%;
38.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.; Gicquel-Sanzey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 82.5; DB
; Pred. No. 0.39;
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (S-D-G-Y)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 82; DB Pred. No. 0.26 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
PIDN:AAK40779.1; GSPDB:GN00155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                 Awayez,
                                                                                                                                                                                                                                                                                                  /ez, M.J.; Cha
H.P.; Redder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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Query Match

18 . 68;

Score

78;

ВВ

2

Length 150;

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-314 <ROM>
                                                                                                                                                                                                                                                                                                                                                               C;Species: Sphingomonas aromaticivorans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Jun-2000
C;Accession: T31220; T31222; T31221
                                                       A; Molecule type: DNA
                                                                                                     A; Accession: T31222
                                                                                                                            A;Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378363; PIDN:AAD03946.1
                                                                                                                                                                                                                                    A; Reference number: A; Accession: T31220
                                                                                                                                                                                                                                                                                 R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W. submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas arom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-318 <OLI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: Z21618
A; Accession: T36991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: strain A3(2)
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, August 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: AL031035; PIDN: CAA19911.1; GSPDB: GN00070; SCOEDB: SC6A9.26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDB.
A;Molecule type: DNA.
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A;Accession: T35457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Murphy, L.; Harris, D.; Parkhill, submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T35457; T36991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Streptomyces coelicolor
C; Date: 05-Nov-1999 #sequence_revision
A;Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378362; PIDN:AAD03945.1
                             A; Residues: 158-314 < RO2>
                                                                             A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                            transposase homolog - Sphingomonas aromaticivorans plasmid pNL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: AL109949; PIDN: CAB52905.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDB.
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Best Local S
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;Gene: SCOEDB:SC6A9.26; SCOEDB:SCJ11.20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 ----EEFVARVAARHARIRELRSEGQSMRAIAAEVGVSVGTVHYAL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 AAEVGVSVGTV----HYALNKNR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 TGRLRLARCVVEDGWPVRRAAERFQVSHTTASRWARRYRQLGVTGMSDRSSRPHHQPRRT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRELNINFNTVLRILKKYNLGKKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
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7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.; Barrell,
July 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-Nov-1999 #text_change 03-Dec-1999
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1.8;
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low affinity penicillin-binding protein 5 (PBP5) - Enterococcus C;Species: Enterococcus faecium C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change C;Accession: S54178 R;Zorzi, W.; Zhou, X.Y.; Raze, D.; Gutmann, L.; Lamotte, J.; Dar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transposase BMEI1423 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AI3429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-115,145-146,'AMLSSRTVP',156,'S' <RO3>
A; Cross-references: EMBL: AF079317; NID: g3378261; PII
C; Genetics:
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten: A;Reference number: AD3252; PMID:11756688
A;Accession: AI3429
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-674 <ZO
                                                    A; Reference number: S54175
A; Accession: S54178
                                                                                                            submitted to the EMBL Data Library,
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A;Introns: 115/3
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A; Status: pre
                                                                                           A; Description: The low affinity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE008917; PIDN:AAL52604.1; PID:g17983423; GSPDB:GN00190
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Best Local S
Matches 28
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Best Local Similarity
Matches 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                          X.Y.; Raze, D.; Gutmann, L.; Lamotte,
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                                                                                         penicillin-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 74.5; DE Pred. No. 2.8; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
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Lzer, P.H.; Hagius, S.; O'Callaghan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
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                                                                                       protein 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 217;
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                                                                                           wild
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                                                                                                                            Coyette,
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A,Molecule type: DNA
A,Residues: 1-139 <KAM>
A;Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB49519.1;
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB2413
A;Gene: PAB2413
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB2413
                                                                                                                                                                                                                                                     hypothetical protein PAB1429 - Pyrococcus abyssi (strain C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_C;Accession: B75055
                                                                C;Genetics:
A;Gene: PAB1429
                                                                                                                                                                       A; Description: Pyrococcus
A; Reference number: A75001
A; Accession: B75055
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                                                                                                                                                                                                                    R; anonymous, Genoscope submitted to the EMBL Data Library, July 1999
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A; Accession: H75179
A; Status: preliminary
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A;Description: Pyrococcus abyssi genome seque
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                                                                                            A;Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50335.1; A;Experimental source: strain Orsay
                                                                                                                              A; Molecule type: DNA
A; Residues: 1-643 <KAW>
                                                                                                                                                         A; Status: preliminary
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Matches 19
Query Match
Best Local Similarity
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Best Local
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17; Conserv
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 72.5;
No. 13;
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A;Residues: 1-673 <ZOR>
A;Cross-references: EMBL:X84B61; NID:g790436;
C;Superfamily: penicillin-binding protein 2B
                                                                                                                                                                                                                                                                                                                                          R;Zorzi, W.; Zhou, X.Y.; Raze, D.; Gutmann, L.; Lamotte, J.; Dardenne, O.; Coyette, J.; submitted to the EMBL Data Library, February 1995
s,Description: The low affinity penicillin-binding protein 5 in wild type and highly per
                                                                                                                                                                                                                                                                                                                                                                                                           low affinity penicillin-binding protein 5 (PBP5) - Enterococcus faecium (fragment) C; Species: Enterococcus faecium C; Date: 08-Jul:1995 #sequence_revision 03-Aug-1995 #text_change 26-May-2000
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A; Description: The low affinity penicillin-binding protein 5 in wild to
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A;Molecule type: DNA
A;Residues: 1-673 <ZOR>
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A; Accession: S54182
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A; Accession: S54175
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                                                                  PKTGDLLALASSPSYDPNKMTNGISQEDYKSYEENPEQPFISRFATGYA-----PGST 418
                                                                                                   PRNGYSIAAAA-----KKL--GVSESTVKRWTSEPREEFVARVAARHARIRELRSEGQS 59
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19; Conser
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Pred. No. 14;
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Pred. No. 14;
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probable IS1617 transposase - Yersinia pestis plasmid pCD1
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T43610; T42913
    C; Accession:
R; Hu, P.; El:
                                                                                                               RESULT 15
T43610
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A;Experimental source: S185
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A;Title: Cloning and sequencing of the low-affinity penicillin-binding protein 3r-enc A;Reference number: A36903; MUID:93259926
A;Accession: A36903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          low-affinity penicillin-binding protein 3r - Enterococcus hirae C;Species: Enterococcus hirae C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
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A36903
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A;Molecule type: DNA
A;Residues: 1-678 <ZOR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Enterococcus faecium C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: sequence extracted from NCBI backbone C; Superfamily: penicillin-binding protein 2B
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A; Residues: 1-678 <PIR>
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Best Local
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Pred. No. 14;
16; Mismatches
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Pred. No. 14;
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  Kobayashi,
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J. Bacteriol. 180, 5192-5202, 1998
A;Title: Structural organization of virulence-associated plasmids of Yersinia pestis.
A;Reference number: 222578; MUID: 8422474
A;Accession: 743610
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross references: EMBL:AF053946; NID:g2996222; PIDN:AAC62592.1; PID:g2996269
A;Cross references: EMBL:AF074612; NID:g3827122
A;Accession: 742913
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 742913
A;Accession: 7
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Perfect score:
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Match
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  GenCore version (c) 1993 - 2000
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RT65_WYXXA
Y013_TREPA
INN2_ECOLI
INN1_ECOLI
YE85_ECOLI
YE85_RABIT
ALFB_RABIT
ALFB_RABIT
ALFB_ECOLI
MOUS_LYTVA
YHJB_ECOLI
ATCU_RHIME
YGUG_YEAST
ALFB_SHEEP
ATC2_RHIME
YDJG_ECOLI
YAST
ALFB_SHEEP
YDJG_ECOLI
YAST
ALFB_SHEEP
YDJG_ECOLI
YAST
AKHI_MAIZE
RPC_BP163
P5CS_CAEEL
RL19_HALMA
UHPA_ECOLI
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ILEU_PIG
MAPB_HUMAN
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P30651
P15238
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P27667
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Q493941
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P52962
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014301
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                                                                                                                                                                       1 myxococcus
7 treponema p
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2 lytechinus
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y sus scrofa
homo sapien
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escherichia
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saccharomyc
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RESULT 2 RT65_MYXXA ID RT65_MYXXA AC P23071; DT 01-NOV-1991 01-NOV-1991 01-NOV-1991 01-NOV-1991 015-DEC-1998
STANDARD;

PRT;

427 AA

(Rel. 20, Created)
(Rel. 20, Last sequence update)
(Rel. 37, Last annotation update)

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3 1	Query Ma Best Loc Matches	EMBL; Inter Pfam; Trans SEQUE	This between the use modden or second	SEQ STR MED Pre "Tr IS9 J.	Shige Bacte Shige NCBI	P3921 01-FI 01-FI 16-OC	RESULT 1 INSN_SHIDY		35 35 35 37 38 39 39 44 42 44 42 45 45 46 46 46 46 46 46 46 46 46 46 46 46 46
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AKKLGVSI : AKAMDVGI	17. Similarity 34. B; Conservative	13; -; NOT IPR002514; 527; Trans le element 112 AA;	PROT enter succession of this security of the	OM N.A. 11546; 1	<pre>dysenteriae. Proteobacteria; D=622;</pre>	(Rel. 31 (Rel. 31 (Rel. 40 insN for	STA		1144.5 1144.5 1144.5 1144.5 1144.5 1144.6 1146.6 11
ESTVKRWT : STMTRWV	17.4% 34.0% vative	X17613; -; NOT_ANNOTATEI PTO; IPRO02514; Transposa PF01527; Transposase_8; posable element; Transposable eleme	y is [nsti: nsti: ins: ins: licentli	PubMed-2 ar M., F Shigella c of the 1090-409 LVED IN		31, Created) 31, Last seq 40, Last ann for insertion	STANDARD:		100 · 1 301 1 308 1 308 1 462 1 848 1 879 1 880 1 232 1 298 1 312 1 414 1
YSIAAAAKKLGVSESTVKRWTSEPREEFVAR- ::	; Scc;	NOT_ANNOTATED_CDS. 514; Transposase_8. ransposase_8; 1. ment; Transposition a; 12739 MW; 7B01	PROT entry is copyright. It e Swiss Institute of Bioinfin Bioinformatics Institute. In Profit institutions as in this statement is not remujures a license agreement email to license@isb-sib.ch	163395; ayet O.; dysente 1S3 gro 9(1990) THE TRAN	gamma sı		D #2	ALJ	YIS1_SHISO YWBI_BACSU LIPA_CHLMU REGB_RHOSH MYSP_DIRIN MYSP_ONCVO MYSP_ONCVO YAGL_ECOLI YM61_HSVI1 YM62_MYCTU YM42_MYCTU YM42_MYCTU YM42_MYCTU YM42_MYCTU
РКА	73; DB 1; No. 0.74; smatches 20	n; DNA-binding 1B52B5E6F8C6A	propropro ticgere as as ht	IN-ATCC 11546; IN-ATCC 11546; INE-90299339; PubMed-2163395; INE-90299339; PubMed-2163395; INSposition in Shigella dysenteriae: isolation in specific the IS3 group of insertion in acteriol. 172:4090-4099(1990). FUNCTION: INVOLVED IN THE TRANSPOSITION OF THE SEQUENCE IS911. SIMILARITY: BELONGS TO THE TRANSPOSASE FAMILY:	subdivision; Ent	ate) pdate) element	112 AA	ALIGNMENTS	SHISO BACSU CHLMU CHLMU CHLMU CHLMU CHLMU CHLMU CHLMU CHLMU CHLMU LHCU LHCU LHCU LHCU LHCU LHCU LHCU LHC
VAARHARIRELRSEGQ 58 : : SPITPEQIEIRELRKKLQ 87	Length 112; ; Indels 6;	recomb	duced through a colla s and the EMBL outs are no restrictions its content is in Usage by and for co tp://www.isb-sib.ch/a	n and analysis n sequences."; HE INSERTION	Enterobacteriaceae	IS911.			P16939 s P39592 b Q9pji2 c Q9pji2 c Q53068 p P13392 d Q02171 o Q01107 e P77607 e Q0116 i Q50683 m Q46607 a
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C 083057;
JT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
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                                                                                Treponema pallidum.
Bacteria; Spirochaetales;
STRAIN-NICHOLS;
MEDLINE-98332770; PubMed-9665876;
Fraser C.M., Norris S.J., Weinsto
                                           SEQUENCE FROM N.A.
                                                                     NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0866; RNADNAPOLMS.
Transferase; RNA-directed RNA
SEQUENCE 427 AA; 48024 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00078; rvt; 1
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OC. NATI. ACAD. SCI. U.S.A. 87:942-945(1990).

- FUNCTION: PARTICIPATES IN THE SYNTHESIS OF A MSDNA (A BRANCHED I LINKED BY A 2',5'-PHOSPHODIESTER LINKAGE TO A SINGLE-STRANDED DI OF UNKNOWN FUNCTION. THE RETRON TRANSCRIPT SERVES AS PRIMER AND TEMPLATE TO THE REACTION, AND CODES FOR THE RT.
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S., Herzer P.J., Inouye M.;
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                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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  Weinstock G.M.,
                                                                                   Spirochaetaceae; Treponema
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  C96436BF86E4D0D7 CRC64;
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  White
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Best Local
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p39212;
01-FEB-1995 (Rel. 3
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16-OCT-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                  STRAIN-K12 / MG1655;
MEDLINE-95334362; PubMed-7610040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
              InterPro; IPR002514; Transposase_8.
Pfam; PF01527; Transposase_8; 1.
                                                                                                        or send an
                                                                                                                     modified and this statement is not removed. entities requires a license agreement (See
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                                                                                                                                                                                                                                                           Nucleic Acids Res. 23:2105-2119(1995).
-!- FUNCTION: INVOLVED IN THE TRANSPOSITION OF
                                                                                                                                                                                                                                                                         "Analysis of the Escherichia coli genome VI: DNA sequence of region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                     Burland V.D., Plunkett
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
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SEQUENCE 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sodergren E.,
                                            EcoGene; EG40014; insN.
                                                          EMBL; AE000499; AAC77239.1;
                                                                        EMBL; U14003; AAA97179.1;
                                                                                                                                                                 the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                       Blattner F.R.;
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McLeod M.P., S
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5E1B311377B49DB2 CRC64;
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                                                                                                                     http://www.isb-sib.ch/announce/
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., Peterson
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element;

Transposition;

DNA-binding; DNA recombination;

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RESULT 5
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Davis R.W.;
Submitted (SEP-1996) to the
SUBMITTION: INVOLVED IN TH
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the Euro
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                                        EMBL; AE000133; AAC73358.1; -.
EMBL; D83536; BAA77925.1; -.
EMBL; U70214; AAB08674.1; ALT_INIT.
ECOGENE; EG40014; InsN.
InterPro; IPR002514; Transposase_8; 1.
Pfam; PF01527; Transposase_8; 1.
                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
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16-OCT-2001 (Rel. 40, Last sequ
01-MAR-2002 (Rel. 41, Last anno
Transposase insN for insertion
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P75679; P71288;
                           Transposable element; Transposition; DNA-binding; DNA recombination;
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Lashkari D., Lew H.,
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European Bioinformatics Institute
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41, Last annotation
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32.1%;
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N., Hyman R., Kalman S., Komp C., Kurdi C
Lin D., Namath A., Oefner P., Roberts D.,
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BF1A0B16CB666AF3 CRC64;
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Kurdi O.,
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16-OCT-2001
                                                                                                                         REPEAT
REPEAT
                                                                                                                                             REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                     Churcher C.M., Gentles S., Barrell B.G., Rajandream M.A., Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 11 WD REPEATS (TRP-ASP DOMAINS).
                                                                                REPEAT
REPEAT
                                                                                                    REPEAT
REPEAT
                                                                                                                                                                                   PROSITE; PS00678; WD_REPEATS_1; FALSE_N PROSITE; PS50082; WD_REPEATS_2; 6. PROSITE; PS50294; WD_REPEATS_REGION; 1.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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Pfam; PF00400; WD40; 9.
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SM00320; WD40; 9.
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Trp-Asp repeats conta
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Score 67.5; I
Pred. No. 15;
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Q28634;
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CDH16.
Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
Yeromorpha; Leporidae;
                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            member of the cadherin multigene fami
J. Biol. Chem. 270:17594-17601(1995)
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DOMAIN
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SIGNAL
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Pfam; PF00028; cadherin; 6.
SMART; SM00112; CA; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation and cDNA cloning of Ksp-cadherin, member of the cadherin multigene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thomson R.B., Igarashi P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95340560; PubMed-7615566;
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BIOI. Chem. 270:17594-17601(1995).

THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN MANUER IN CONNECTING CELLS; CADHERINS MAY THUS SORTING OF HETEROGENEOUS CELL TYPES.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: KIDNEY-SPECIFICITED TO MEMBRANES OF RENAL TUBULAR EPITHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
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CADHERIN 6.
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01-NOV-1997 (Rel. 35, Last sequence up
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Fructose-bisphosphate aldolase B (EC 4
ALDOB OR ALDB.
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Eukaryota; Metazoa; Chordata; C
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Mammalia; Eutheria; Lagomorpha;
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SIMILARITY: BELONGS TO CLASS I FRUCTOSE-BISPHOSPHATE ALDOLASE
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QRIVANGKGILAADESVGTMGNRLQRIKVENTEENRRQFREILFTVDNSINQSIGGVILF 79
                                           ERLPRNGYSIAAAKKLGVSESTVKRW----TSEPREEF----
                                                                                                         Similarity
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PS00158; ALDOLASE_CLASS_I; 1.
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0 BY SIMILARITY.
55 C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
146 C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
229 SCHIFF-BASE WITH DIHYDROXYACETONE-P.
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                                                                                Score 66; DB
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14; Mismatches
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OA7185A72E89F436 CRC64;
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4.1.2.13) (Liver-type aldolase).
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21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
Fructose-bisphosphate aldolase B (EC 4.1.2.
                                                                                                                  EMBL;
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Hori K., Ishikawa K.;
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or send an email t
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsutsumi K., Mukai T., Tsutsumi R., Mori M
Yatsuki H., Hori K., Ishikawa K.;
"Nucleotide sequence of rat liver aldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-85054935; PubMed=6094564;
MEDLINE-85054935; PubMed=6094564;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure and genomic organization J. Mol. Biol. 181:153-160(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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                                                                    SL; M10149; AAA40716.1; -
SL; X02284; CAA26156.1; -
SL; X02285; CAA26156.1; J
SL; X02287; CAA26156.1; J
SL; X02288; CAA26156.1; J
SL; X02289; CAA26156.1; J
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SL; X02299; CAA26156.1; J
SL; X02299; CAA26156.1; J
SL; X02291; CAA26156.1; J
SL; X02291; CAA26156.1; J
SL; Y01223; CAA24533.1; -
R; A22585; ADRTB.
R; A22585; ADRTB.
SP, P00883; IADO.
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                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute. The by non-profit institutions as longified and this statement is not removed. Ities requires a license agreement (See send an email to license@isb-sib.ch).
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the Swiss Institute of Bioinformatics and the matter are no rest.

There are no rest.
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HETLYQKDSQGKLFRNILKEKGIVVG
PPro; IPR000741; Aldolase_I.
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m; PD001128; Aldolase_I; 1.
TE; PS00158; ALDOLASE_CLASS_I;
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Sciurognathi; Muridae;
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4.1.2.13)
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RESULT
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Best Local 9
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P52962;
01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                        Bachman E.S., McClay D.R.;

"Characterization of moesin in the sea urchin Lytechinus variegatus:
"Characterization to the plasma membrane following fertilization is
inhibited by cytochalasin B.";
J. Cell Sci. 108:161-171(1995).
-I- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
STRUCTURES TO THE PLASMA MEMBRANE.
-I- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyase; So INIT_MET BINDING BINDING BINDING BINDING ACT_SITE
                                                                                                 Pfam;
                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are n use by non-profit institutions as long as its c modified and this statement is not removed. Usage entities requires a license agreement (See http://worsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-95256329;
           Structural protein; Cy
DOMAIN 58 224
                              PROSITE; PS00660; BAND_41_1;
PROSITE; PS00661; BAND_41_2;
PROSITE; PS50057; BAND_41_3;
                                                                PRINTS; PR00935; BAND41.
SMART; SM00295; B41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Moesin.
                                                                                                                                   EMBL; U14180; AAC46514.1;
                                                                                                                                                                                                                                                                                                                                                                                             Echinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                   Lytechinus
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                                                                                                              InterPro;
                                                                                                                        InterPro; IPR000299;
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                                                                                       PF00769; ERM; 1.
                                                                                                  PF00373; Band_41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schiff
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363 .
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Echinodermata; Eleutherozoa; Echinozoa;
oidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycolysis; Multigene
                     Cytoskeleton
67579 MW;
                                                                                                           Ezrin_radixin_moesin
                                                                                                                        Band_4.1.
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25.6%;
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C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
SCHIFF-BASE WITH DHYDROXYACETONE-P.
ESSENTIAL FOR ENHANCED ACTIVITY OF THE
ENZYME TOWARD FRUCTOSE 1,6-BISPHOSPHATE
AS COMPARED WITH FRUCTOSE 1-PHOSPHATE.
           BAND
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 E1BA3F8E84B5E764
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8EF4F3E621E6DD9A
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RESULT 11
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U00039; AAB18496.1; -.
EMBL; AE000428; AAC76545.1; -.
HSSP; P10957; IRNL.
ECOGene; EG12246; yhjB.
InterPro; IPR000792; HTH_LuxR.
Pfam; PF00196; GerE; 1.
PRINTS; PR00038; HTHLUXR.
SMART; SM00421; HTH_LUXR; 1.
                                                                                                                                                                                                                                                                                                           Hypotheticar Complete proteome.
159 178 H
170 AA; 22604 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00622; HTH_LUXR_FAMILY; 1.
Hypothetical protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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MEDLINE-94316500; PubMed-8041620;
Sofia H.J., Burland V., Daniels D.L., Plur
Sofia H.J., Burland V., Daniels D.L., Plur
"Analysis of the Escherichia coli genome.
"Analysis of the 81.5 minutes.";
region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
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188 NRTQA 192
                                                                                                   128
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                                                NRTDA 85
                                                                                                WRTTPEKDIKDLKSLSARQREILTMLAAGESNKEIGRALNISTGTVKAHLESLYRRLEVK 187
                                                                                                                                                WTSEPREEF -- VARVAARHARIRELRSEGQSMRAIAAEVGVSVGTVHYALN------
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Pred. No. 8.7;
12; Mismatches
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ATCU_RHIME
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Pfam; PF00403; HMA; 2.

Pfam; PF00702; Hydrolase; 1.

PF1NTS; PR00119; CATATPASE.

PRINTS; PR00940; CATPATPASEA.

PRINTS; PR00941; CATPATPASE

PRINTS; PR00941; CATPATPASE

PRINTS; PR00946; HGSCAVENGER.

PROSITE; PS00154; ATPASE_E1_E2; 1.

PROSITE; PS010147; HMA_1; 2.

PROSITE; PS01046; HMA_2; 2.

Hydrolase; Transmembrane; Phosphorylation; Marketal-Liditor; Corporation of the company of the 
Metal-binding; C.
TRANSMEM 174
TRANSMEM 210
TRANSMEM 248
TRANSMEM 271
RANSMEM 458 4
NSMEM 541 56
NSMEM 569 58:
SMEM 773 793
MEM 775 815
1 16 81
1 16 81
1 1 83 149
2 9 29
3 93
9 3 93
9 6 96
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Q9XSX3;

Q9XSX3;

30-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last seq

01-MAR-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reeve W.G., Tiwari R.P., Kale N.B., Dilworth M.J., Glenn A.R., "The role of copper and P-type ATPase in the acid-tolerance of Rhizobium leguminosarum by viciae and Sinorhizobium meliloti.", Submitted (FEB-199) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN COPPER TRANSPORT (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + H(2)0 - ADP + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF129004; AAD27639.1; -. HSSP; Q04656; 1AW0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPP
(E1-E2 ATPASES). SUBPAMILY IB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 2 HMA DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : IPR001802; |
: IPR001934; |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              656; 1AW0.
IPR001366; Cad_ATPase.
IPR000579; Cat_P_ATPas
IPR001757; E1-E2_ATPas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cat_P_ATPaseA.; E1-E2_ATPase.; HG_scavenger.
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PHOSPHORYLATION (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Magnesium; ATP-binding;
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                SIMILARITY).
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RESULT 14
ALFB_SHEEP
ID ALFB_SHEEP
AC P52210;
DT 01-OCT-1996
DT 01-OCT-1996
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Best Local
P52210;
01-OCT-1996
01-OCT-1996
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METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 18.1 kDa protein in MDS3-GCN1 intergenic region.
YGL196W OR G1315.
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-S288C / FY1679;
MEDLINE-97197971; PubMed-9046087;
Coglievina M., Klima R., Bertani I.,
                                                                                                                                                                                                                                             EMBL; Z72718; CAA96908.1; -.
EMBL; X91837; CAA62948.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P53095;
01-0CT-1996
                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 165 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                Yeast 13:55-64(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequencing of a 40.5 kb fragment located on the chromosome VII from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-S288C / FY1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                   112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast)
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                                                                                                                         3 TRERLPRNGYSIAAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELRS 55
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| NDAPALAEADVGIAVGT 733
                                                                                                  TREASSIKGFGICADLEHVLKSESFSREW-----YVARVSQEHGILRPIRN
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                                                                                                                                                              Similarity
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23; Conservative
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718
827
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                                       STANDARD;
 34, Created)
34, Last sequence
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718
86239
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Pred.
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Pred.
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MAGNESIUM (BY SIMILARITY).
707E2148DDDA5004 CRC64;
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No. 8;
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                                                                                                                                                                         Length 165;
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                                                                                                                                                                                                                                                                                                                                                a collaboration -
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RESULT 15
ATC2_RHIME
ID ATC2_RHIME
AC P58342;
DT 01-MAR-2002
DT 01-MAR-2002
DT 01-MAR-2002
DE Copper-trans
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00274; glycolytic_enzy; 1. ProDom; PD001128; Aldolase_I; 1. PROSITE; PS00158; ALDOLASE_CLASS_I; 1. Lyase; Schiff base; Glycolysis; Multig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a control between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: SIXTH STEP IN GLYCOLYSIS.

-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY),

-!- MISCELLANEOUS: IN VERTEBRATES, THREE FORMS OF THIS UB
GLYCOLYTIC ENZYME ARE FOUND, ALDOLASE A IN MUSCLE, AL
LIVER, & ALDOLASE C IN BRAIN.

-!- SIMILARITY: BELONGS TO CLASS I FRUCTOSE-BISPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 1219:223-227(1994).
-!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate phosphate + D-glyceraldehyde 3-phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
Bovidae; Caprinae; (
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALDOB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z29372; CAA82563.1; HSSP; P00883; 1ADO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Mesonephros;
MEDLINE-94368863; PubMed-8086469;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aldolase B from fetal mesonephros."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Last annotation update)
Fructose-bisphosphate aldolase B (EC 4.1.2.13) (Liver-type aldolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                78
                                                                                                                                                                          45 ARHARIRELRSEGQSMRAIAAEVGVSVG
                                                                                                                                                                                                      18
                                                                                                                                                                                                                                   ω
                                                                                                                                                                                                                                   TRERLPRNGYSIAAAAKKLGVSESTVKRW----TSEPREEF---
                                                                                                                                               LFHETLYQKDGQGKLFRDILKEKGIVVG
                                                                                                                                                                                                      TARRIVANGKGILAADESVGTMGNRLQRIKVENTEENRRQFRELLFTVDSSVSQSIGGVI 77
                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000741; Aldolase_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L., Pailhoux E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Sheep).
                                                                                                                                                                                                                                                                                                                                      363
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(Rel. 41, Created)
(Rel. 41, Last sequence up)
(Rel. 41, Last annotation)
(Rel. 41, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                 55
146
229
363
                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                      AA;
                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                  ; Glycolysis; Multigene family.

0 BY SIMILARITY.

55 C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
146 C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
229 SCHIFF-BASE WITH DIHYDROXYACETONE-P.
363 ENSYMIAL FOR ENHANCED ACTIVITY OF THE
ENZYME TOWARD FRUCTOSE 1,6-BISPHOSPHATE
AS COMPARED WITH FRUCTOSE 1-PHOSPHATE.
39500 MW; FC8B45666821EZBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ovis.
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                                                                                                                                                                                                                                                                          15.2%;
25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                              Pred. No. 20;
3; Mismatches
                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bezard J.,
                                                                         PRT;
                                                                                                                                                                                                                                                                            No.
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6 outstation
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Copper-transporting

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                  METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL603645; CAC49418.1; -.
PROSITE; PS00154; ATPASE_E1_E2; 1.
PROSITE; PS01047; HMA_1; 2.
PROSITE; PS50846; HMA_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                          MOD_RES
                                                                                                                                                                                               METAL
METAL
                                                                                                                                                                                                                                 DOMAIN
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                               Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - I - SIMILARITY: CONTAINS 2 HMA DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21396508; PubMed=11481431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTP2 OR ATCU2 OR RB1018 OR SMB21578.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                           PRANSMEM
                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Transmembrane;
                                                                                                                                                                                                                                                                     TRANSMEM
                                            670
717 NDAPALAEADVGIAVGT
                       65
                                                                    10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein (By similarity). SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (E1-E2 ATPASES). SUBFAMILY
                    -----AEVGVSVGT 73
                                            NRRTAEAIARKLGI-------DEVVAEVLPEGKVEAIRKLRQGGRSVAFIGDGI 716
                                                                 NGYSIAAAAKKLGVSESTVKRWTSEPREEFVARV--AARHARIRELRSEGQSMRAIA---
                                                                                           23;
                                                                                                                                                  430
458
771
797
16
83
26
29
93
93
94
718
827
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                            Copper;
                                                                                                                                                  718 M
85861 MW;
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26
29
29
93
714
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478
793
819
                                                                                                    15.2%;
                                                                                                                                                                                                                                                                                                                                                            Repeat;
                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation; Magnesium; ATP-binding;
                                                                                           11; Mismatches
                                                                                                                                                COPPER (POTENTIAL).
COPPER (POTENTIAL).
COPPER (POTENTIAL).
COPPER (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                    Score 64; DB 1; Length 827; Pred. No. 47;
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POTENTIAL.
POTENTIAL.
POTENTIAL.
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